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Identification of potential vectors of *Xylella fastidiosa* in Portuguese olive orchards and weeds

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Resumo alargado

Xylella fastidiosa Wells et al. é uma fitobactéria gram-negativa, estritamente aeróbia, restrita ao xilema, com cinco subespécies conhecidas, nomeadamente *X. fastidiosa* subsp. *fastidiosa*, *X. fastidiosa* subsp. *multiplex*, *X. fastidiosa* subsp. *pauca*, *X. fastidiosa* subsp. *morus* e *X. fastidiosa* subsp. *sandyi*. A sua transmissão ocorre através de insetos picadores-sugadores do xilema e, até a data, são conhecidas mais de 560 espécies hospedeiras da bactéria, distribuídas por mais de 260 géneros e 80 famílias. As dez famílias com maior número de espécies de plantas suscetíveis são, em ordem decrescente: Fabaceae, Asteraceae, Vitaceae, Poaceae, Rosaceae, Rutaceae, Fagaceae, Rubiaceae, Lamiaceae e Oleaceae. As principais doenças provocadas por *X. fastidiosa*, em termos de importância económica, são a Doença de Pierce, na vinha, a Clorose Variegada dos Citros, em citrinos, o "Almond Leaf Scorch", em amendoeira, a "Peach Phony Disease" em pessegueiro e o Declínio Súbito do Olival, em oliveira, entre outras.

A transmissão da bactéria é um processo progressivo que inclui três passos: (i) aquisição pelo vetor de uma planta infetada (ii) fixação e retenção na cutícula do estomódeo do vetor, onde a bactéria forma uma espécie de biofilme, e (iii) inoculação numa nova planta hospedeira. À medida que a população bacteriana cresce na planta saudável pode ocorrer o bloqueio de vasos xilémicos, devido à sua agregação através da formação de um biofilme, desencadeando respostas na planta, como por exemplo o aparecimento de tilos, reduzindo o fluxo de água e sais minerais. No entanto, uma transmissão bem-sucedida de *X. fastidiosa* depende de vários fatores, como por exemplo, a espécie e o comportamento de vetor – como as preferências de local de alimentação na planta, a planta hospedeira e a subespécie da bactéria. Também a ecologia, as alterações climáticas, a sazonalidade e as práticas de gestão da cultura são igualmente fatores relevantes. Todavia, é importante notar que não há especificidade entre o par vetor-fitopatógeno, visto que os insetos vetores podem transmitir todos os genótipos de *X. fastidiosa*.

Tal como referido, *X. fastidiosa* é transmitida por insetos com armadura bucal picadora-sugadora, que se alimentam da seiva xilémica (Hemiptera: Auchenorrhyncha), o que parece ser o único requisito para a competência do vetor, tornando largo o espectro de potenciais vetores. No entanto, nem todos os potenciais vetores têm um papel significativo na transmissão da bactéria, pois outros fatores influenciam a sua propagação, nomeadamente o habitat, o hospedeiro e sua interação com os vetores, a mobilidade dos vetores e a sua distribuição. As espécies de vetores, atuais e potenciais, de *X. fastidiosa* presentes na Europa encontram-se distribuídas pelas seguintes famílias/subfamílias: Aphrophoridae (27 espécies), Cercopidae (7 espécies), Cicadidae (61 espécies), Cicadellinae (5 espécies) e Evacantinae (3 espécies). Atendendo à sua ampla distribuição e frequência, algumas das espécies mais relevantes são: *Philaenus spumarius* Linnaeus, *Cicadella viridis* Linnaeus, *Aphrophora alni* Fallén e *Aphrophora salicina* Goeze.

Sendo uma bactéria endémica nas Américas, foi já reportada em Taiwan, Irão, Israel e em alguns países europeus. No ano de 2013, ocorreu a primeira confirmação de *X. fastidiosa* na Europa, na região da Apúlia (sul da Itália), onde a bactéria foi responsável pela destruição de milhares de hectares de oliveiras. Desde então, as prospeções anuais nacionais obrigatórias nos Estados-Membros da União Europeia levaram à descoberta de surtos de *X. fastidiosa* em vários países, como por exemplo em França, Alemanha, Espanha e, em 2018, Portugal. O fitopatógenio foi detetado no município de Vila Nova de Gaia, em plantas de lavanda (*Lavandula dentata* Linnaeus) no jardim do Zoo Santo Inácio. Desde essa primeira deteção verificaram-se pelo menos 84 focos, tanto em jardins públicos, como em jardins privados.

Portugal é um dos quatro maiores produtores de azeite, a seguir a Espanha, Itália e Grécia, possuindo a cultura da oliveira grande significância cultural e económica, especialmente na região do Alentejo, que é responsável por 70% da produção nacional de azeitona. A importância da olivicultura em Portugal e as consequências devastadoras da propagação de *X. fastidiosa* nos olivais italianos, evidenciam o

potencial risco de contaminação desta cultura pela bactéria. Dessa forma as medidas de gestão adequadas para limitar a ocorrência da bactéria dependem em grande parte do conhecimento local dos seus potenciais vetores e da sua dinâmica, sendo imperativo o estudo da sua ocorrência nos olivais desta região.

Face ao exposto, o objetivo deste estudo consistiu na prospeção de potenciais insetos vetores de *X. fastidiosa* no Alentejo, em olivais livres de produtos fitofarmacêuticos, como contributo para a construção de um mapa de risco e subsequente plano de monitorização contínua dos vetores, elementos úteis para limitar a ocorrência do declínio súbito do olival em olivais da região. A amostragem ocorreu entre 3 de maio e 8 de junho de 2017 na região do Alentejo, a qual foi dividida em 18 unidades geográficas (UGs) de 30 × 30 km, onde sete olivais sem aplicação de inseticidas por UG foram selecionados para prospeção, resultando num total de 126 pontos de amostragem. Em cada ponto de amostragem, os artrópodes foram capturados em oliveiras e vegetação rasteira circundante com um aspirador de artrópodes. Os Auchenorrhyncha foram separados e identificados até ao nível taxonómico mais baixo possível. No caso dos adultos, quando não foi possível a determinação da espécie, foram consideradas morfoespécies. Posteriormente, foram efetuados testes moleculares para detetar a presença de *X. fastidiosa* em potenciais vetores. Procedeu-se, também, à avaliação do efeito de 22 variáveis independentes na abundância dos vetores de *X. fastidiosa*, por análise de variância não paramétrica (teste de Kruskal-Wallis) para identificar diferenças estatisticamente significativas associadas a essas variáveis. Na presença de diferenças significativas ($p<0.05$), os dados posteriormente ranqueados das variáveis foram discriminados pelo teste *post hoc* de diferenças mínimas significativas (LSD).

Foram triadas 300 amostras recolhidas na Região do Alentejo, das quais 99 em oliveira, 21 na vegetação rasteira mista e 180 em espécies vegetais individuais. No total foram coletados 39 527 artrópodes (incluindo adultos e estágios imaturos), dos quais 11 022 eram Hemiptera e destes 1 145 eram Auchenorrhyncha. De todos os Auchenorrhyncha, 954 indivíduos eram da infra-ordem Cicadomorpha e 191 pertenciam à infra-ordem Fulgoromorpha.

Os resultados demostraram que apesar de *X. fastidiosa* ainda não ter sido detetada na Região do Alentejo, cinco vetores / vetores potenciais estão presentes na área de estudo, nomeadamente, *Philaenus spumarius*, *Philaenus tesselatus* Melichar, *Cercopis intermedia* Kirschbaum, *Lepyronia coleoptrata* (Linnaeus) e *Neophilaenus campestris* (Fallén). De acordo com os resultados obtidos, *P. tesselatus* foi a espécie de cigarrinha-de-espuma mais comum, com uma ampla distribuição na Região do Alentejo. Apenas um indivíduo masculino de *P. spumarius* e um indivíduo feminino de *C. intermedia* foram encontrados neste estudo. *Neophilaenus campestris* embora presente em baixa abundância, representa uma ameaça potencial para a cultura da oliveira e para as culturas circundantes, uma vez que a sua capacidade de transmissão foi comprovada por outros autores. Tendo isso em consideração, deve-se realizar um plano de monitorização contínua destes vetores/ potenciais vetores na Região do Alentejo, em especial foco nas espécies de *P. spumarius*, *P. tesselatus* e *N. campestris*.

A identificação dos vetores, possibilitou também observar uma clara diferença na morfologia do edeago do *P. spumarius* e *P. tesselatus*, especialmente nos apêndices superiores e inferiores, com *P. tesselatus* exibindo medidas sempre maiores do que *P. spumarius*.

Nenhuma diferença foi observada na preferência da planta hospedeira pelos vetores, exceto para *Philaenus* sp., que apresentou maior abundância na vegetação herbácea do que na oliveira. Assim, os estratos herbáceos presentes na região devem ser submetidos a prospeção e, se a presença destes indivíduos se tornar crítica, os estratos devem ser removidos. Especial atenção deve ser dada às famílias de plantas onde os insetos vetores foram mais abundantes ou às famílias mais vulneráveis à bactéria, especialmente Asteraceae, Apiaceae (*Daucus carota* Linnaeus, *Conium maculatum* Linnaeus) e Convolvulaceae (*Convolvulus arvensis* Linnaeus).

Foram capturadas várias outras espécies de Auchenorrhyncha que são vetores de outras doenças. Identificou-se também dois indivíduos de *Arocephalus punctum* (Flor) neste estudo, sendo que tanto quanto é do conhecimento da autora, este é o primeiro relato desta cigarrinha em Portugal. Além disso, foram encontrados onze indivíduos de Auchenorrhyncha parasitados, com a maioria parasitados por Dryinidae (Hymenoptera). Novos estudos devem ser realizados para verificar se Dryinidae pode, de facto, parasitar cigarrinhas bem como, estudos de identificação de inimigos naturais de vetores nos olivais alentejanos, as suas relações ecológicas e se a gestão dos inimigos naturais pode contribuir para o controlo biológico dos vetores de *X. fastidiosa*.

Por fim, foi demonstrado que na área de estudo a temperatura e a precipitação desempenham um papel significativo na abundância de *Philaenus* spp. *Philaenus tesselatus* apresentou diferenças significativas na abundância face à precipitação total e *Philaenus* sp. em relação à temperatura média, com a sua maior abundância a registar-se a 24 °C. Isto significa que as alterações climáticas futuras são um elemento com impacto na epidemiologia do declínio súbito do olival na Região do Alentejo, visto que podem influenciar a distribuição e as dinâmicas populacionais de potenciais vetores, o crescimento das plantas hospedeiras, a eficiência da transmissão da bactéria e as relações vetor/planta hospedeira.

Palavras-chave: declínio súbito do olival; fitopatógeno; gestão de pragas; *Neophilaenus campestris*; *Philaenus*;

Abstract

Xylella fastidiosa Wells et al. is a xylem-limited phytopathogen, originating in America and transmitted by sap-sucking insects. The current database on *X. fastidiosa* host plants includes more than 560 species distributed by more than 260 genera and 80 families.

The emergence of the bacterium throughout Europe and its first report in Portugal in 2018, with at least 84 detections in Portugal to date, showed that the phytopathogen is spreading at an alarming rate. Considering the spreading rate, the economic and cultural significance of olive culture in Portugal, and the devastating consequences in Italian olive groves, it is pertinent to know the presence of capable vectors and host plants of the bacterium in Alentejo olive groves.

This study aims to survey the presence of vector species of *X. fastidiosa,* during spring, in traditional Alentejo olive orchards and to contribute to a continuous monitoring plan of vectors, thus preventing or limiting the occurrence of olive quick decline syndrome.

The results showed that, despite the phytopathogen has not been detected in the Alentejo Region, five vector species were present, *Philaenus spumarius* Linnaeus, *Philaenus tesselatus* Melichar, *Cercopis intermedia* Kirschbaum, *Lepyronia coleoptrata* (Linnaeus) e *Neophilaenus campestris* (Fallén). *Philaenus tesselatus* was the most abundant species, however only one individual of *P. spumarius* and *C. intermedia* were found. Also, although present in low abundance in this study, *N. campestris* represents a potential threat to olive culture and surrounding areas since its transmission ability has been demonstrated. Taking this into consideration, the continuous monitoring plant should focus on *P. spumarius*, *P. tesselatus* and *N. campestris*.

No difference was observed in host plant preference by vectors, except for *Philaenus* sp., which showed significantly higher abundance on ground cover that on olive trees. Nevertheless, the herbaceous strata present in the region should also be subjected to prospection and, if the situation becomes critical, should be removed. Special attention must be payed to families were the insect vectors found were most abundant or to the families that are vulnerable to the bacterium, specially Asteraceae, Apiaceae (*Daucus carota* Linnaeus, *Conium maculatum* Linnaeus) and Convolvulaceae (*Convolvulus arvensis* Linnaeus).

Multiple Auchenorrhyncha species that are vectors of other plant diseases were captured. Two individuals of *Arocephalus punctum* (Flor) were found in this study, which to the author's knowledge, may be the first report of this leafhopper in Portugal. Also, eleven parasitized Auchenorrhyncha individuals were found, with most of parasitized specimens parasitized by Dryinidae (Hymenoptera).

Finally, in the study area, climatic variables played a significant role in the abundance of *Philaenus* spp. Statistical analysis showed that total precipitation and mean temperature had a significant effect on *P. tesselatus* and *Philaenus* sp. abundance, respectively.

The conditions in Alentejo Region are very suitable for the establishment and spread of *X. fastidiosa* and future climate change could impact the epidemiology of olive quick decline syndrome in the region, since climatic variables influence the distribution and dynamics of vector populations, the host plants growth, the efficiency of pathogen transmission and vector/host plant dynamics.

Key-words: *Neophilaenus campestris*; olive quick decline syndrome; pest management; *Philaenus*; phytopathogen;

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Cq – Quantification cycle

CTAB – Cetyl Trimethyl Ammonium Bromide

CVC – Citrus Variegated Chlorosis

FLA – Flavicollis

GU – Geographic Unit

IDW – Inverse Distance Weighting

IPMA – Instituto Potuguês do Mar e da Atmosfera

MAR – Marginellus

MAR/FLA – Marginellus/Flavicollis

NAC - N-Acetylcysteine

OQDS – Olive Quick Decline Syndrome

PBO – Pyrethrin + Piperonyl Butoxide

PD – Pierce's Disease

POP – Populi

qPCR – Quantitative Polymerase Chain Reaction

TRI – Trilineatus

TYP – Typicus

USA – United States of America

1. Introduction

1.1. Biological invasion

In the course of increasing worldwide travels of the human species, we exert a powerful changing force, capable not only to alter environments but also to mould new ones. As we migrate, we do not only bring the "material trappings of our culture" but also transport species with us, sometimes with our knowledge, other times, often in the case of microorganisms, without it. The introduction of foreign species to new habitats can have potential devastating ecological and economic consequences (Vitousek et al., 1996).

Biological invasions, in general, involve several countries. One country is the source of a range of species and that country is linked to others through the movement of goods and people. Different countries have different governments which in their territories enforce different laws or similar laws in different capacity. Meaning that, the level of biological control exercised in one country can directly influence the risk of invasion of others. Efforts of the international control of biological invasions are often uncoordinated, since it is done individually by countries, generating a higher risk of invasion spread (Perrings et al., 2002).

One relevant and current example is the introduction and emergence of the phytopathogen *Xylella fastidiosa* Wells et al. in Europe, a bacterium endemic to the Americas that colonizes the xylem vessels (water transport system composed of dead, lignified cells) of host plants. This pathogen is transmitted by insect vectors, more specifically xylem-sap feeding specialists (Hemiptera: Auchenorrhyncha) (Janse & Obradovic, 2010; Redak et al., 2004) and is responsible for multiple diseases affecting relevant agricultural and forest plant species.

1.2. *Xylella fastidiosa* diversity and host plant specificity

Xylella fastidiosa is a Gram-negative, strictly aerobic, xylem-limited, non-flagellated bacterium with a growth optimum of 26-28 °C (Janse & Obradovic, 2010). Considering the genetic data available, there are five accepted subspecies of *X. fastidiosa*, namely *X. fastidiosa* subsp. *fastidiosa*, *X. fastidiosa* subsp. *multiplex*, *X. fastidiosa* subsp. *pauca*, *X. fastidiosa* subsp. *morus* and *X. fastidiosa* subsp. *sandyi* (Nunney et al., 2014; Schaad et al., 2004; Schuenzel et al., 2005). It is widely accepted that *X. fastidiosa* subsp. *fastidiosa*, *X. fastidiosa* subsp. *multiplex* and *X. fastidiosa* subsp. *pauca* are allopatric in origin (Sicard et al., 2018), but the origin of *X. fastidiosa* subsp. *sandyi* is still debated (Almeida & Nunney, 2015), with some studies suggesting it is within *X. fastidiosa* subsp. *fastidiosa* variation range (Jacques et al. 2016; Marcelletti & Scortichini, 2016). Regarding *X. fastidiosa* subsp. *morus*, Vanhove et al. (2019) revealed this subspecies does not appear to be the result of large-scale genome-wide recombination between *X. fastidiosa* subsp. *fastidiosa* and *X. fastidiosa* subsp. *multiplex*, as initially hypothesized by Nunney et al. (2014), although this question should be addressed in more detail in future studies.

Xylella fastidiosa has been isolated mainly from economically relevant plant species and this sampling bias may be limiting its current known genetic diversity. The isolation of the bacterium from usually unstudied plants may give insights into *X. fastidiosa* phylogenetic relationships and help to clarify the species history and validity of the currently accepted subspecies.

Host specificity within *X. fastidiosa* subspecies is variable, with different subspecies and strains being able to infect different ranges of host plants (Almeida & Nunney, 2015). *Xylella fastidiosa* subsp. *fastidiosa* originated in Central America and causes disease in grapevine and almond, among other plants (EFSA PLH et al., 2019; Sicard et al., 2018). *Xylella fastidiosa* subsp. *multiplex* originated in North America and causes disease in a wide range of trees, including almond, peach, plum, oak trees,

shade tree and grapevine (EFSA PLH et al., 2019; Nunney et al., 2012). With origin in South America, *X. fastidiosa* subsp. *pauca* causes disease in citrus, coffee, grapevine, olive trees and ornamental plants (EFSA PLH et al., 2019; Loconsole et al., 2016). *Xylella fastidiosa* subsp. *sandyi* infects oleander, as well as grapevine and almond (EFSA PLH et al., 2019; Nunney et al., 2012). Lastly, *X. fastidiosa* subsp. *morus* has been found to infect mulberry and blueberry (EFSA PLH et al., 2019).

1.3. *Xylella fastidiosa* distribution

The phytopathogen *X. fastidiosa* is endemic to the Americas and is widespread throughout North, Central e South America (Almeida & Nunney, 2015). The disease caused by *X. fastidiosa* was first reported in 1892, by Newton Pierce in South California, at the time named as California vine disease, devastating the grape industry in the region (Pierce, 1892). The disease was later renamed as Pierce´s disease (PD) and remains a problem in California today (Tumber at al., 2014). The bacterium persisted as a pathogen of interest exclusive to the United States of America (USA) until 1987, when it emerged in Minas Gerais (Brazil) linked to citrus variegated chlorosis (CVC) on sweet orange trees (Chang *et al*., 1993).

For many years, reports of the bacterium remained confined to the Americas, but in the 2000s, *X. fastidiosa* subsp. *fastidiosa* was reported in Asia causing PD in Taiwanese vineyards. More recently, in 2014, the bacterium was also found in several provinces of Iran associated to almond and grapevine (**Figure 1.1**) (Amanifar, 2014; Su et al., 2013). The latest report on the presence of *X. fastidiosa* subsp. *fastidiosa* occurred in July 2019, in Hula Valley (north-eastern Israel) where symptomatic almond trees were discovered in three adjacent commercial orchards (**Figure 1.1**) (EPPO, 2019c).

The first confirmed report of *X. fastidiosa* subsp. *pauca* ST53 in Europe occurred in 2013, in Apulia, (southern Italy) where the bacterium was killing thousands of ha of olive trees (Saponari et al., 2013). Since then, annual mandatory national surveys in European Union Member States lead to the discovery of *X. fastidiosa* outbreaks in multiple countries. The phytobacterium has been reported in Corsica and mainland France (Alpes-Maritimes) (*X. fastidiosa* subsp. *multiplex*, *pauca* and *fastidiosa*) in 2015 (Denancé et al., 2017). In 2016, it was detected in Germany, although this was an isolated case in a greenhouse that has been officially declared as eradicated in 2018 (**Figure 1.1**) (EPPO, 2018). In the same year, the phytopathogen was also detected in Spain, more specifically in the Balearic Islands. This time, multiple subspecies were present: *X. fastidiosa* subsp. *fastidiosa* (Mallorca), *X. fastidiosa* subsp. *multiplex* (Mallorca and Menorca), and *X. fastidiosa* subsp. *pauca* (Ibiza) (EPPO, 2017). Later, in 2017, the Spanish authorities notified the presence of *X. fastidiosa* subsp. *multiplex* in almond orchards from Alicante (Autonomous Region of Valencia, mainland Spain) (EPPO, 2019a). The detection of multiple subspecies of the bacterium associated to the outbreaks in Europe, leads to conclude that multiple introductions occurred throughout time but remained unnoticed and that *X. fastidiosa* emergence in the region is not as recent as it is usually mentioned (Denancé et al., 2017; Landa, 2017). Lastly, in 2018 the presence of *X. fastidiosa* subsp. *multiplex* was reported in Madrid (mainland Spain) associated to olive trees (**Figure 1.1**) (EFSA PLH et al., 2019). Also, in 2018, the phytopathogen was found in the region of Tuscany. This was the first time *X. fastidiosa* subsp. *multiplex* was detected in Italy (**Figure 1.1**) (Marchi et al., 2018). Until that moment, only *X. fastidiosa* subsp. *pauca* ST53 (EFSA PLH, 2016) was present in Italy. The detection of a new subspecies is evidence for a new introduction of the bacterium in Italy.

The bacterium (*X. fastidiosa* subsp. *multiplex* ST7) was first detected in Portugal in December 2018, in the municipality of Vila Nova de Gaia (near Porto) in a composite and asymptomatic sample of lavender (*Lavandula dentata* Linnaeus) collected in a zoo (**Figure 1.1**) (EPPO, 2019b). After first detection,

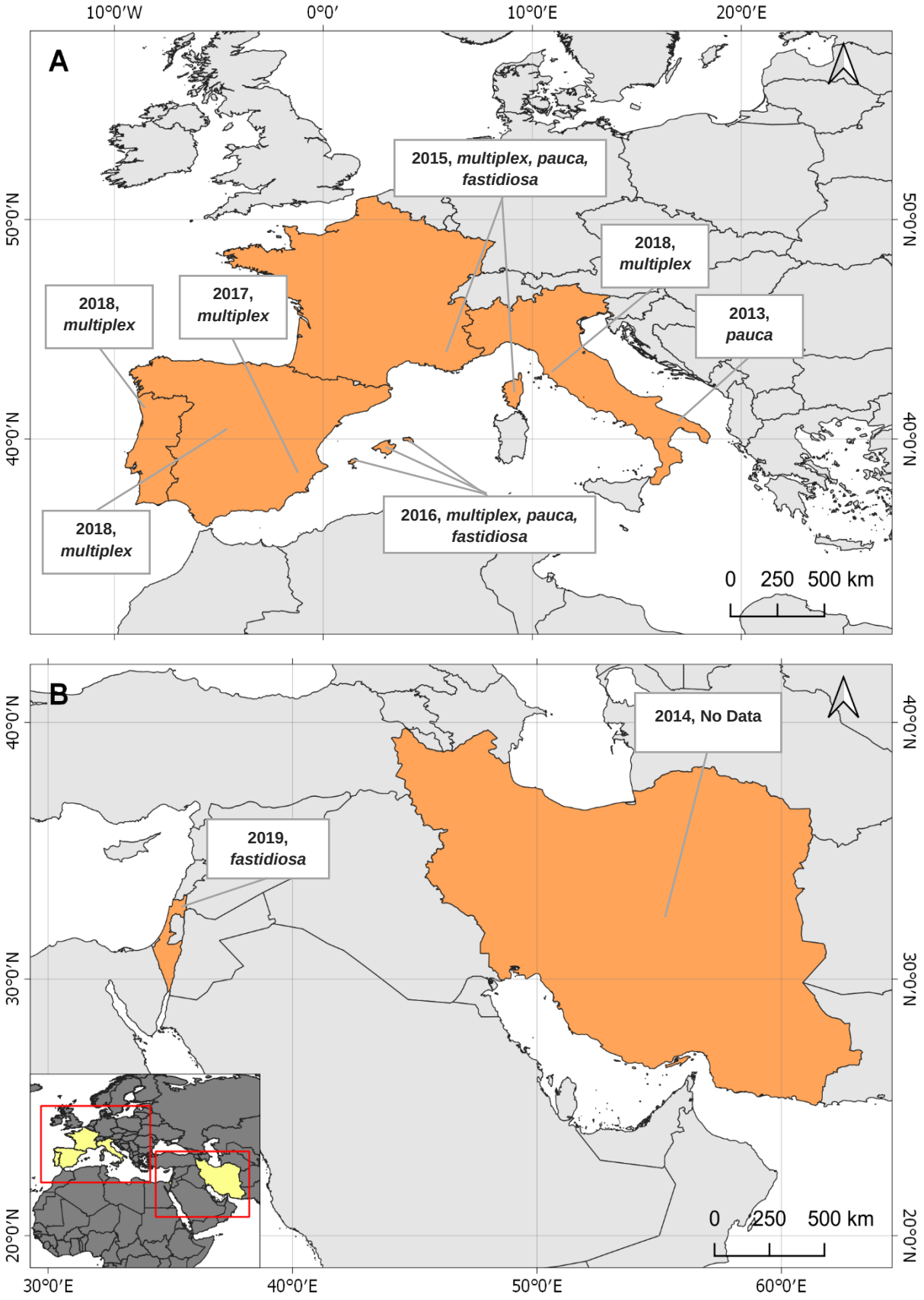

Figure 1.1 - Geographic distribution of *Xylella fastidiosa* in Europe (**A**) and in the Middle East (**B**), with respective year of first detection and present *X. fastidiosa* subspecies. Maps projected in WGS84.

immediate prospection of the infected area revealed other contaminated flower beds of *L. dentata* and *Lavandula angustifolia* Miller. About 1 km from the initial focus, infected plants of several ornamental

species in a non-commercial nursery were discovered. Now, with continuous prospection, at least 84 infection foci were discovered, both in public, as well as in private gardens, resulting in successive enlargements of the "Demarcated Area" comprising the "Infected Areas", including all the vegetables that are in a radius of 50m around the contaminated plants and a "Buffer Zone" surrounding a 2.5 km radius (DRE, 2020). The large number of detections, after initial discovery and posterior prospection probably means that *X. fastidiosa* have been present in Portugal for quite some time.

1.4. Host plants

The current database on *X. fastidiosa* host plants includes more than 560 species distributed by more than 260 genera and 80 families. The 10 families with the largest numbers of *X. fastidiosa*-susceptible plant species are, in descending order: Fabaceae, Asteraceae, Vitaceae, Poaceae, Rosaceae, Rutaceae, Fagaceae, Rubiaceae, Lamiaceae and Oleaceae (EFSA, 2018). When considering *X. fastidiosa* host plant species confirmed by at least two detection methods, the number of host species goes down to around 312. Nonetheless, the numbers of known plant hosts are constantly rising, as new reports continue to appear, especially now that this phytopathogen seems to be disseminated in the Mediterranean region.

Although the phytopathogen can infect a vast number of plant species, not all of them have disease symptoms or economic significance. The most economically important diseases caused by *X. fastidiosa* are PD, leaf scorch of almond and coffee, CVC, phone peach disease (**Figure 1.2**) and olive quick decline syndrome (OQDS) (**Figure 1.3**) (Hopkins & Purcell, 2002; Janse & Obradovic, 2010; Martelli et al., 2016).

Disease development is not immediate due to the fastidious bacterium growth and it may take months to years for a plant to display any visible symptom (Purcell & Saunders, 1999). The systemic infection by the phytopathogen presents itself in a range of disease symptoms that may vary between plants, but often resemble water stress or nutrient deficiencies (EFSA PLH, 2015). On OQDS, the symptoms in early stages of infection include the presence of leaf scorch and scattered desiccation of twigs and small branches, prevailing on the upper part of the canopy. As the infection progresses, these symptoms become more severe and are extended to the rest of the canopy, which then acquires a burnt look. Even if the tree is heavily pruned, to favour new growth, it is flimsy and desiccates in a short while (**Figure 1.3**). If the roots are still viable, the withered and weakened trees do not die immediately and may produce abundant suckers from the base as they try to recover, surviving for some time (Martelli et al., 2016).

1.5. Vector diversity

As a xylem-limited bacterium, *X. fastidiosa* is exclusively transmitted by xylem sap-feeding specialists, which seems to be the only requirement for vector competence (Janse & Obradovic, 2010; Redak et al., 2004). As so, all xylem fluid-feeding insects must be considered as potential vectors (EFSA et al., 2019).

Multiple transmission trials involving phloem sap-feeding specialists such as *Macrosteles fascifrons* (Stål) and *Euscelidius variegatus* (Kirschbaum) (Cidadellidae: Deltocephalinae) or *Agalmatium bilobum* (Fieber) (Fulgoromorpha: Issidae) having been consistently negative (Cavalieri et al., 2019; Elbeaino et al., 2014; Severin, 1949). Some species of phloem sap-feeding specialists like *Euscelis lineolatus* Brullé (Cicadellidae: Deltocephalinae) or *Latilica tunetana* (Matsumura) (Issidae) have tested positive for *X. fastidiosa*, which means they can occasionally contact with xylem sap and successfully acquire the bacterium, but they were never successful to transmit the phytopathogen (Cavalieri et al., 2019; Elbeaino et al., 2014).

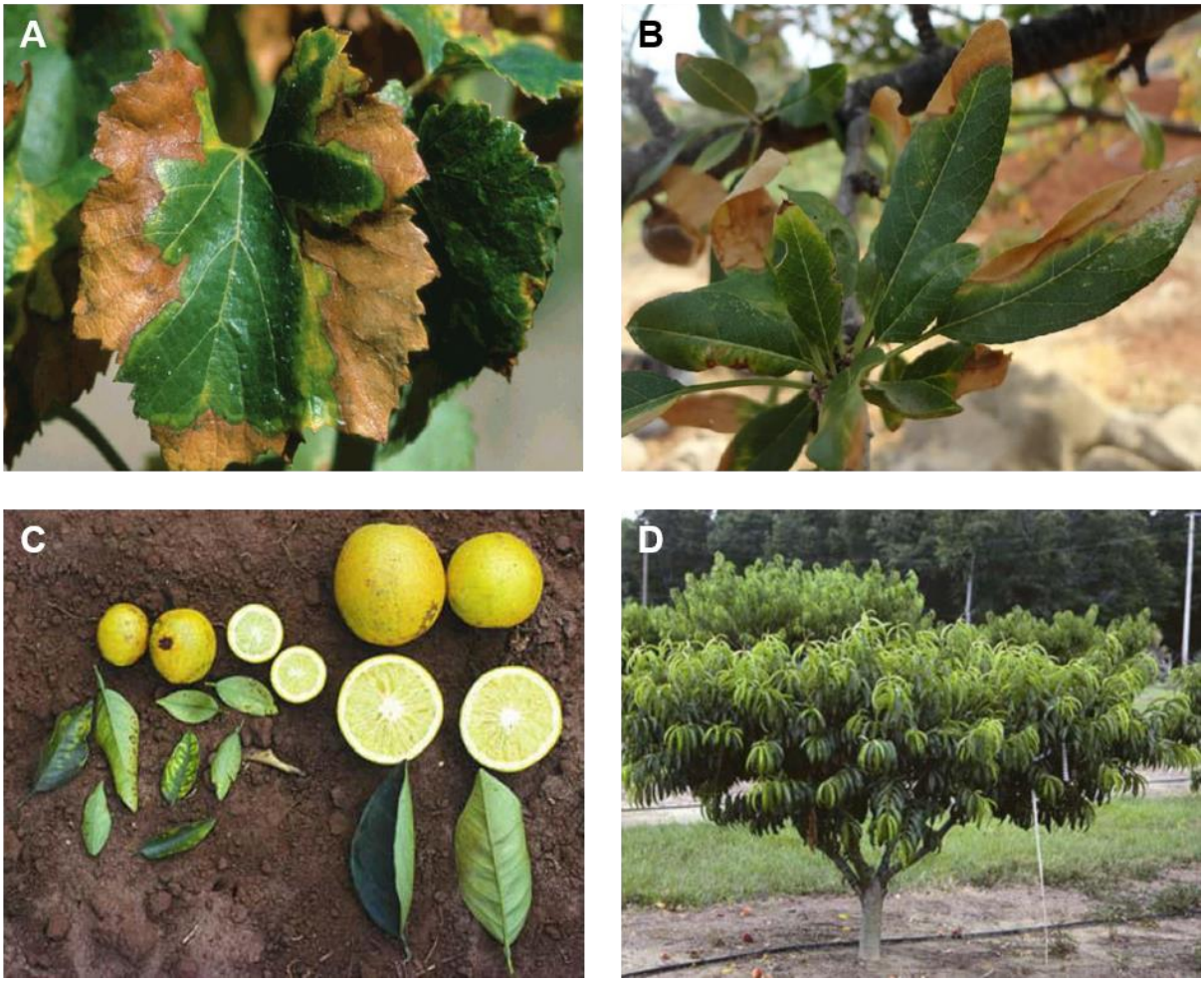

Figure 1.2 – Symptoms of *Xylella fastidiosa* in diferent host plans. **A** – Leaf marginal necrosis of Pierce's disease of grapevine. **B** – Almond leaf scorch. **C** – Chlorotic leaf lesions and small fruit symptoms of citrus variegated chlorosis on the left, healthy citrus leaves and fruit on the right. **D** – Phony peach disease, stunted tree with dwarfed new growth and shortened stem internodes. Sources: A – Janse & Obradovic (2010); B – IPSP CNR (2017); C and D – Hopkins & Purcell (2002).

Xylem-sap feeding specialists are distributed among multiple families within the sub-order Auchenorrhyncha (Hemiptera), and include all spittlebugs/ froghoppers (Cercopoidea), all cicadas (Cicadoidea) and sharpshooter leafhoppers (Membracoidea: Cicadellidae: Cicadellinae) (Stancanelli et al., 2015). The plant tissue feeding preferences are unknown for some leafhopper groups and some authors have proposed Evacanthinae and Mileewinae (Cicadellidae), two subfamilies closely related to Cicadellinae, could also be xylem sap-feeding specialists (Tonkyn & Whitcomb, 1987). There is some evidence for that since *Friscanus friscanus* (Ball) and *Pagaronia furcata* Oman (Evacanthinae: Pagaroniini) are competent vectors of *X. fastidiosa*, associated to PD in California according to Nielson (1968).

Some of the main vectors of the phytopathogen in North America, responsible for the spread of PD are *Graphocephala atropunctata* (Signoret) and *Homalodisca vitripennis* (Germar), whereas in South America the main vectors of CVC comprise *Bucephalogonia xanthophis* (Berg), *Dilobopterus costalimai* Young, *Acrogonia citrina* Marucci & Cavichioli, *Oncomeopia facialis* (Signoret) and *Macugonalia leucomelas* (Walker) (Almeida et al., 2005a; Cavalieri & Porcelli., 2017; Janse & Obradovic, 2010; Miranda et al., 2009; Yamamoto & Gravena, 2000) (**Table 1.1**). There are reports of spittlebugs and cicadas as vectors in the Americas (Krell et al., 2007; Paião et al., 2002), but the role played by cicadas *X. fastidiosa* transmission and disease epidemics is not understood and yet to be proven (EFSA et al., 2019).

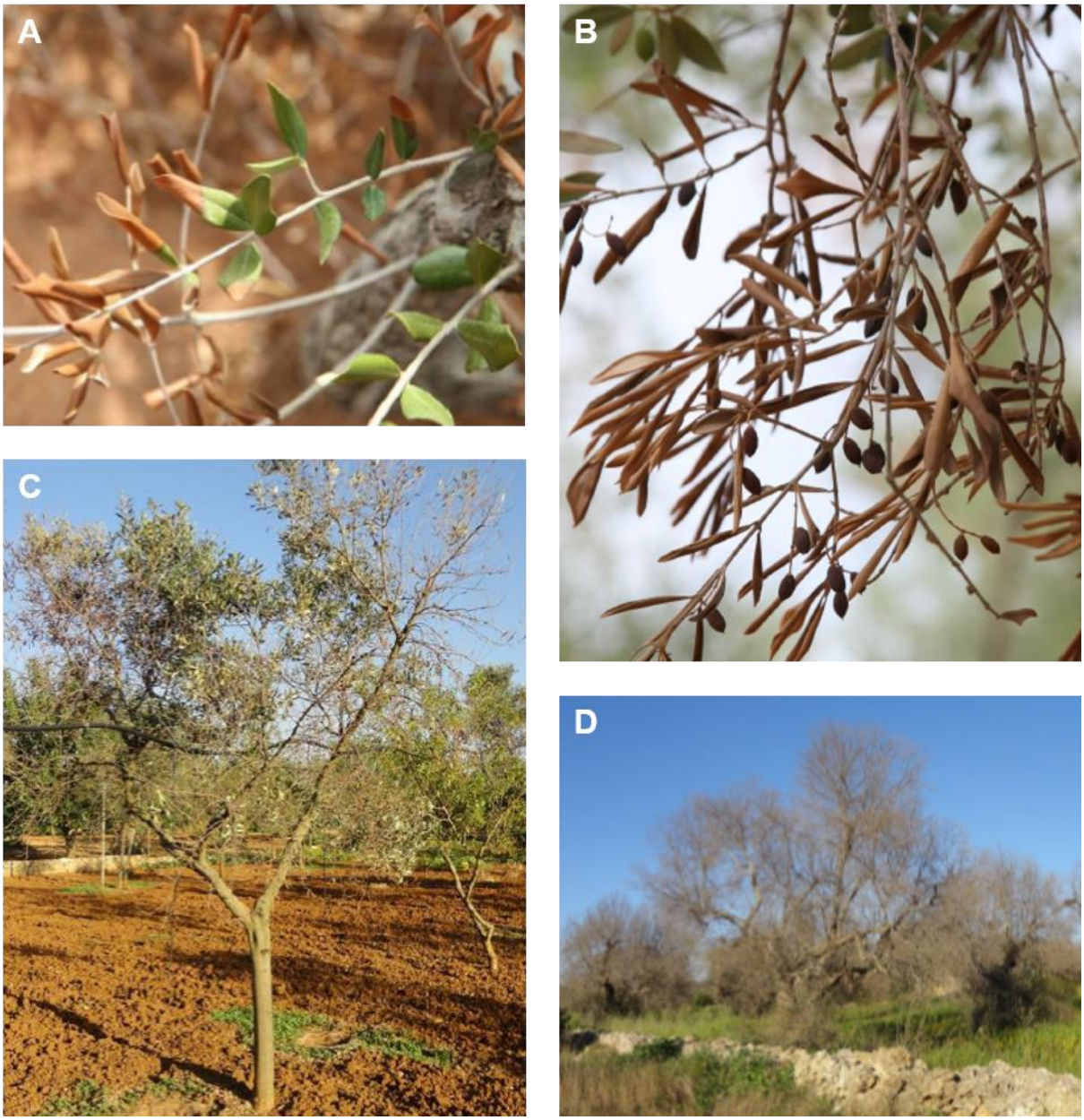

Figure 1.3 – Symptoms of olive quick decline syndrome. **A** – Initial leaf scorch; **B** – Intermediate stage of infection, desiccation of branches; **C** – Extensive desiccation on young tree; **D** – Quick decline syndrome at an advanced stage. Source: IPSP CNR (2017).

The groups of current and potential vector species of *X. fastidiosa* present in Europe are Aphrophoridae (27 species), Cercopidae (7 species), Cicadidae (54 species), Cicadellinae (5 species) and Evacantinae (3 species) (Bosco, 2014; EFSA, 2013; Stancanelli et al., 2015). Due to their widespread distribution and commonness, some of the most relevant species comprise: *Philaenus spumarius* Linnaeus, *Cicadella viridis* Linnaeus, *Aphrophora alni* Fallén and *Aphrophora salicina* Goeze (Bosco, 2014; Janse & Obradovic, 2010; Stancanelli et al., 2015) (**Table 1.2**).

There is limited information regarding habitat, ecology and phenology of European Evacanthinae, such as *Evacanthus interruptus* Linnaeus or *Evacanthus acuminatus* (Fabricius). Nevertheless, there is significant information available regarding the phenology and ecology of "the two main species of Cicadellinae present in Europe", *C. viridis* and *Graphocephala fennahi* Young (EFSA et al., 2019).

The information about European spittlebugs is also lacking, but some interesting data on the host plants and insect life cycles are available for species of the genera *Aphrophora*, *Cercopis* and *Neophilaenus*. (Cavalieri & Porcelli., 2017, EFSA et al., 2019; Elbeaino et al., 2014).

The key vectors of *X. fastidiosa* in the American continent are sharpshooters, where they are a highly diverse group, but in Europe this group is limited to a few uncommon species with restricted distribution ranges, except for *C. viridis*.

All the American vector species are absent from Europe according to the Fauna Europaea Database, except for *P. spumarius* which has been identified as the key vector in Apulia, Italy (Elbeaino et al., 2014). *Philaenus spumarius* was the only confirmed vector of *X. fastidiosa* in Europe until recently (Cavalieri & Porcelli, 2017), when a study of vector-mediated transmissions conducted by Cavalieri et al. (2019) demonstrated transmission ability for two additional spittlebug species, namely *Philaenus italosignus* Drosopoulos & Remane and *Neophilaenus campestris* (Fallén). These two spittlebugs are competent vectors of the strain *X. fastidiosa* subsp. *pauca* ST53 associated with the severe OQDS epidemics in Apulia (southern Italy). Furthermore, Bodino et al. (2019a) demonstrated that *C. viridis* is also a competent, though inefficient, vector of *X. fastidiosa* subsp. *pauca* ST53 to periwinkle, despite successful acquisition and transmission occurred only from artificial diet and with very low efficiency and no success at transmission was observed from periwinkle to periwinkle. More transmission trials should be conducted, with more individuals and different host plants to understand the low transmission efficiency of *X. fastidiosa* by the insect.

Table 1.1 - Vectors of *X. fastidiosa* in the Americas: main insect groups and most important vector species.

Superfamilies	Family	Subfamily	Main species	Role as a vector	Author's
Cercopoidea	Aphrophoridade	Aphrophorinae	*Philaenus spumarius* (Linnaeus)	North America Low	EFSA, 2013; Stancanelli et al., 2015
Membracoidea	Cicadellidae	Cicadellinae	*Acrogonia citrina* Marucci & Cavichioli	South America Citrus variegated chlorosis	EFSA, 2013; Stancanelli et al., 2015
			Bucephalogonia xanthophis (Berg)	South America Citrus variegated chlorosis	Bosco, 2014; EFSA, 2013; Stancanelli et al., 2015
			Dilobopterus costalimai Young	South America Citrus variegated chlorosis	Bosco, 2014; EFSA, 2013; Stancanelli et al., 2015
			Graphocephala atropunctata (Signoret)	North America Pierce´s disease	Bosco, 2014; EFSA, 2013; Stancanelli et al., 2015
			Homalodisca vitripennis (Germar)	North America Pierce´s disease	Bosco, 2014; EFSA, 2013; Stancanelli et al., 2015
			Macugonalia leucomelas (Walker)	South America Citrus variegated chlorosis	EFSA, 2013; Stancanelli et al., 2015
			Oncomeopia facialis (Signoret)	South America Citrus variegated chlorosis	EFSA, 2013; Stancanelli et al., 2015

Table 1.2 - Current and potential vector species of *X. fastidiosa* in Europe: main insect groups and most important potential vector species.

Superfamilies	Family	Subfamily	Main species	Role as a vector	Author's
Cercopoidea	Aphrophoridade (27 species)	Aphrophorinae	*Aphrophora alni* Fallen	Potential vector	Stancanelli et al., 2015; Bosco, 2014
			Aphrophora salicina Goeze	Potential vector	Stancanelli et al., 2015; Bosco, 2014
			Neophilaenus campestris (Fallén)	Confirmed vector	Cavalieri et al. (2019); EFSA, 2013
			Philaenus spumarius (Linnaeus)	Confirmed vector	Cavalieri & Porcelli, 2017; EFSA, 2013; Elbeaino et al., 2014; Stancanelli et al., 2015
			Philaenus italosignus Drosopoulos & Remane	Confirmed vector	Cavalieri et al. (2019); EFSA, 2013
			Philaenus tesselatus Melichar	Potential vector	EFSA, 2013
	Cercopidae (7 species)	Cercopinae	*Cercopis vulnerata* Rossi	Potential vector	Bosco, 2014; Stancanelli et al., 2015
Cicadoidea	Cicadidae (54 species)	Cicadinae	*Cicadatra atra* (Olivier)	Potential vector	Bosco, 2014; Stancanelli et al., 2015
Membracoidea	Cicadellidae (8 species)	Cicadellinae (5 species)	*Cicadella viridis* (Linnaeus)	Competent, though inefficient vector	Bodino et al. (2019a); EFSA et al., 2019
			Graphocephala fennahi Young	Potential vector	EFSA, 2013; EFSA et al., 2019
		Evacantinae (3 species)	*Evacanthus acuminatus* (Fabricius)	Potential vector	EFSA, 2013
			Evacanthus rostagnoi (Picco)	Potential vector	EFSA, 2013

1.6. Phytopathogen transmission

As indicated above, *X. fastidiosa* is a xylem-inhabiting bacterium transmitted by xylem-fluid feeding insects (Hemiptera, Auchenorrhyncha). The transmission occurs as follows: (i) acquisition by the vector from a source plant; (ii) attachment and retention to vector's foregut cuticle; (iii) detachment and inoculation into a new plant host (Janse & Obradovic, 2010).

Xylella fastidiosa plant colonization is a progressive process. Xylem-vessels are interconnected by adjoin pits that allow the passage of xylem sap but block the passage of larger objects due to the presence of the pit membrane. This membrane, acts as a porous filter, allowing the passage of water and nutrients while restricting the passage of air bubbles, pathogens, and particles between the adjacent xylem vessels (Choat et al., 2003; Crombie et al., 1985). As the bacterial population grows, blockage of individual vessels by the formation of biofilm-like colonies may occur, triggering plant responses (like tyloses), thus reducing sap flow in the xylem vessels. Within-plant spread among xylem vessels occurs via pit membrane (Baccari & Lindow, 2011; Newman et al., 2003).

Similarly, and yet differently, *X. fastidiosa* also forms a biofilm on the cuticular foregut of insect vectors. Although biofilm formation may be a characteristic of the colonizing process, it is not necessary for a successful transmission, as evidenced by the absence of a detectable latent period. This means that inoculation may occur instantly after acquisition, before the biofilm has been formed (Almeida et al., 2005a; Sicard et al., 2018).

Within the insect vectors, the bacterium is restricted to the alimentary canal, more specifically the pre-cibarium and cibarium (parts of the foregut) and does not systemically infect the insect body (non-circulative). *Xylella fastidiosa* retention place within its vectors implies that vectors lose infectivity with moulting, as the foregut is of ectodermal origin and is renewed with moulting and means that there is no transstadial and transovarial transmission (Almeida et al., 2005a). As such, newly emerged adults must feed on an infected plant to become infectious, but, once infected, adult vectors can transmit during their whole lifetime (persistent transmission) (Almeida et al., 2005a; EFSA PLH, 2015). This is possible because of their unique sucking mouthparts (mandibular and maxillary stylets) that allow them to reach the xylem of their host plants, from which they ingest sap. Owing to the very poor nutritional value of xylem fluid, xylem fluid feeders consume large amounts of sap, ingesting other microorganisms present there (EFSA PLH, 2015). Almeida et al. (2005b) showed active vector behaviour is required for inoculation of bacterial cells into plants, instead of just a passive transfer promoted by the xylem tension within the plants as previously hypothesised, yet the specific behaviour involved in phytopathogen inoculation is yet to be determined (Almeida & Nunney, 2015).

A successful *X. fastidiosa* transmission is impacted by several factors, such as vector species, host plant, pathogen strain (Redak et al. 2004), as well as vector behaviour such as within-plant feeding site preferences (Daugherty et al. 2010), but ecology, climate change, seasonality and crop-management practices are also relevant (Sicard et al., 2018).

Also, it is important to note that there is no vector-pathogen specificity, the insect vectors can transmit all *X. fastidiosa* genotypes (Almeida & Nunney, 2015).

1.7. Disease spread

Local spread of *Xylella fastidiosa* is mainly driven through transmission by the present vectors. *Xylella fastidiosa* can be locally propagated in different ways, specifically by primary or secondary spread, meaning that epidemiology may vary in different cultures and regions or both. These two kinds of disease spread mechanisms are not mutually exclusive but the prevalence of one kind over another dictates the potential success of certain management measures.

Primary spread is defined when disease occurs is mainly transmitted by infected vectors from outside the culture (vineyard, olive, citrus groves), while secondary spread is when the proliferation occurs within the plot (from tree-to-tree) (Almeida at al., 2005). For example, in the case of the outbreak in the Apulia, Italy, both primary infection and secondary spread occurred, with the latter prevailing. This is supported by a study conducted by Cornara et al. (2017), where all the individuals collected from December 2013 to May 2014, on herbaceous plants, within and outside the olive orchard, tested negative for the bacterium (only one *N. campestris* collected on oleander collected on July 2014). During May, June and July, the populations of individuals increased in olive trees while decreasing in wild plants and weeds (as the ground vegetation became drier). During May 2014, the first *P. spumarius* positive for *X. fastidiosa* were collected from olive canopies. From the end of July, the individuals began to migrate to wild plants and weeds. Simultaneously, the proportion of infected spittlebugs in wild plants and weeds, previously negative, started to increase. Also, the experiments demonstrated that the *P. spumarius* transmitted the bacterium from infected to uninfected olive plants (olive-to-olive). These findings

suggest that the *X. fastidiosa*-infected olive trees are the main bacterial source within olive orchards and that *P. spumarius* a major driver for secondary spread in Italian olive orchards. The spread of Pierce´s disease in vineyards in San Joaquin Valley, Kern County, California appears to occur mainly by primary spread, from outside the culture, rather than by the secondary spread, vine-to-vine, within vineyards. Park et al. (2011) noted that the spatial distribution of *X. fastidiosa*-infected vines in the majority of vineyard blocks studied (12 out of 16) showed evidence of primary spread. Five of those vineyard blocks showed a gradient, where disease incidence decreased with distance to the surrounding environment, also known as the edge effect or spatial trend. The remaining blocks showed a random pattern of PD incidence, also consistent with primary spread of a *X. fastidiosa* vector able to fly long distances into the vineyards.

The main form of CVC proliferation in São Paulo, Brazil is via secondary spread (citrus-to-citrus), since the spatial distribution of symptomatic trees within orange orchards appeared random at first, becoming clustered as the disease incidence increased in the culture (Roberto et al., 2002).

1.8. Control methods

According to the EFSA Plant Health Panel, no treatment is currently available to cure diseased plants and, most often, plants that are contaminated remain infected throughout their life or collapse quickly (EFSA, 2019). The first line of defence against the spread of *X. fastidiosa* is implementing quarantine measures that can prevent the introduction of the bacterium to other regions. In the European Union, this implies establishing eradication areas, buffer zones, and a mandatory phytosanitary passport. Meaning that specified plants which have been grown for at least part of their life in an infected area (eradication area and buffer zone) by the bacterium "shall only be moved to and within the Union territory, if they are accompanied by a plant passport prepared and issued in accordance with Commission Directive 92/105/EEC" (EC, 2015). Considering the wide range of hosts, vectors, environmental conditions, and the global plant trade it is not surprising that the methods described above are not enough by themselves (Janse & Obradovic, 2010). After the introduction occurs, there are several and different methods to contain and/or eradicate the bacterium. These control methods, more specifically chemical, biological and physical control methods, have been extensively studied, but it is important to note that, since the disease dynamics may wary between cultures and regions, the management strategy should vary accordingly to increase its efficiency.

The most widely used control method for insect vectors of *X. fastidiosa* rely on the use of systemic neonicotinoids. The systemic neonicotinoids imidacloprid and dinotefuran are effective insecticides for long-term management of glassy-winged sharpshooter populations (Byrne & Toscano, 2009). However, the honeybee colony collapse linked to sub-lethal exposure of neonicotinoids, imidacloprid or clothianidin (Lu et al., 2014), resulted in a two-year ban of clothianidin, thiamethoxam and imidacloprid by the European Commission (EC, 2013). Recently, of 29 May 2018, the European Commission prohibited all outdoor uses of clothianidin, thiamethoxam and imidacloprid. The appropriate use of this substances is restricted to permanent greenhouses and requires that the resulting crop stays its entire life cycle within a permanent greenhouse, so that it is not replanted outside. Also, seeds treated with these neonicotinoids are prohibited to be placed on the market or used, except where the seeds are intended to be used only in permanent greenhouses and the resulting crop stays in a permanent greenhouse during its entire life cycle (EC, 2018a, 2018b, 2018c). Taking the nefarious effects of systemic neonicotinoids into account, alternative control methods should be considered.

Recently, Dáder et al. (2019) proposed an effective alternative to neonicotinoids, such as pyrethroids (delthamethrin and λ-cyhalothrin), sulfoxaflor and natural pyrethrin + piperonyl butoxide (PBO) for vectors' control. The synergist PBO prolongs its action and enhances its efficacy, being non-toxic alone

regardless of the concentration used. The study results showed these chemical compounds were successful in controlling *P. spumarius* nymphs under laboratory conditions. Pyrethroids (delthamethrin and λ-cyhalothrin) and natural pyrethrin + PBO were associated to higher mortality rates (above 86% after 24h of exposure) than sulfoxaflor, that reached a mortality rate a little over 60% after 24h of exposure. Natural pyrethrin can be a good environmentally friendly option to traditional pesticides, however when it was applied alone the mortality rate only reached 23%, meaning that it should be applied together with PBO for more efficacy.

Regarding biological control, Das et al. (2015) first demonstrated the efficacy and benefits of the application of a cocktail composed of four virulent (Sano, Salvo, Prado and Paz) bacteriophages. The phage cocktail prevented PD symptom development and reduced the pathogen levels in grapevines. Considering the potential applications of the bacteriophages, Bhowmick et al. (2016) studied the transmission of a phage (Paz) by glassy-winged sharpshooters to cowpea plants, assessing the ability of the vectors to acquire and transfer the phage. *Homalodisca vitripennis* were highly efficient in acquiring the phage when it was present in high concentration in plants, but they were unable to transfer phages to other plants efficiently. It was hypothesised that low transfer of the phage by the vectors was due to an apparent dilution effect associated to the feeding activity.

Also, biological control with a benign strain (weak in virulence) of *X. fastidiosa*, EB92-1, could be an environmentally friendly control of the bacterium in the future. The weakly virulent strains produce only minor symptoms in the host as they move and multiply more slowly (Hao et al., 2017; Hopkins, 2005). The EB92-1 strain, showed to reduce the ability of the virulent native PD strains to cause disease, present lower symptom development and mortality rate at the end of the trials (Hopkins, 2005; 2014). On the other hand, Hao et al. (2017) assessed the capacity of the avirulent *X. fastidiosa* strain DPD1311 to protect against the phytopathogen. The inoculations performed in this study were similar to those performed with *X. fastidiosa* EB92-1 to suppress PD (Hopkins, 2005). The grapevines were inoculated with (i) DPD1311, 2 weeks prior to TM1 (wild-type *X. fastidiosa* Temecula 1); (ii) with both strains simultaneously (DPD1311 and TM1); and (iii) with each strain alone. The results showed that a reduction of disease incidence occurred in vines inoculated with DPD1311 prior to TM1, while the vines inoculated with both strains showed no statistical significance when compared with the TM1-only treatment. When comparing the disease severity, TM1-inoculated and TM1+DPD1311-inoculated vines developed disease at a similar rate, showing no significant differences. Contrary to the average disease ratings on plants inoculated with DPD1311 2 weeks prior to TM1 remained significantly lower than those of the other treatments for the duration of the experiment. Considering the findings above, biological control with weakly virulent/avirulent strains could have the potential to reduce the severity of PD in grapevines. Although, the recombination between the genotypes present in the EU and any new genotypes should be considered as it could lead to "new pathogen variants" and perhaps new diseases (EFSA PLH Panel, 2015).

Baccari et al. (2019) studied the potential of an endophytic bacterium, *Paraburkholderia phytofirmans* PsJN (Sessitsch et al.) Sawana et al., to colonise grapevines and interfere with PD caused by *X. fastidiosa*. Surprisingly the endophytic bacterium was able to grow and multiply in the vines. The results showed that when *X. fastidiosa* and *P. phytofirmans* where co-inoculated in the same plant, great reduction of leave scorch symptoms were observed when compared with the control (*X. fastidiosa* inoculated alone in the plants), showing also smaller population sizes of *X. fastidiosa*, as only a few viable cells were recovered from the co-inoculated plants. It is notable, that the reduction of the disease symptoms occurred not only when the strain was co-inoculated with the pathogen in the same site but also when they were inoculated at the same time in different sites of the plant. The authors also tested

and determined that spray inoculation was as effective as needle puncturing, indicating that strain PsJN could be effective as a biological control agent of PD and be easily applied by spraying.

Rolshausen et al. (2018), as well, explored the use of grape endophytic microorganisms as a control agent for PD. After evaluation, two most abundant bacteria inhabiting grapevine xylem were chosen, namely *Pseudomonas fluorescens* (Flügge) Migula and *Achromobacter xylosoxidans* Yabuuchi & Yano. As well as fungi *Cochliobolus* sp. and *Cryptococcus* sp. Result identified both bacteria and *Cryptococcus* sp. were able to reduce PD symptoms development and pathogen concentration in plants, when introduced by either through vacuum infiltration of grape cuttings before the rooting stage or needle inoculation of shoots. Though, when applied by foliar spray or drench application no mitigation of PD symptoms where observed, suggesting that these organisms must be introduced to the xylem to be active. *Cochliobolus* sp. and posteriorly *Curvularia lunata* (Wakker) Boedjin were used to isolate radicinin, anti-*X. fastidiosa* fungal natural product. The authors demonstrated that purified radicinin inhibited pathogen growth in a dose-dependent manner by targeting protease activity. Regrettably, and as mentioned above, foliar sprays of radicinin did not reduce PD severity, the authors theorized that this was due to of low penetration of the active compound in the plant xylem. More studies must be conducted to evaluate the efficiency of this anti-fungal product.

Biological control of the insect vectors focuses mainly on egg-parasitoids such as those from the genera *Gonatocerus* (Hymenoptera: Mymaridae) (Son et al., 2012; Triapitsyn et al. 2002) and *Oligosita* (Hymenoptera: Trichogrammatidae) (Triapitsyn & Shih, 2014), among others. Recently, Mesmin et al. (2019), provided a first report of *Ooctonus vulgatus* Haliday (Hymenoptera: Mymaridae) as a potential biocontrol agent of *P. spumarius* in Europe. Furthermore, the endoparasitoid *Verrallia aucta* Fallén (Diptera: Pipunculidae) is known for attacking adults of *Neophilaenus lineatus* (Linnaeus), *N. campestris* and *P. spumarius* (Whittaker, 1969).

Possible genetic control of *X. fastidiosa* consists in regulating the growth of the bacterium (reducing biofilm formation and ability to adhere to surfaces) by altering the expression of *rpfF* gene which encodes the synthase for diffusible signal factor (Lindow et al., 2014).

Good potential has been shown by the N-Acetylcysteine (NAC), a cysteine analogue used mainly to treat human diseases. The molecule successfully reversed the symptoms of *X. fastidiosa* infection, by reducing biofilm formation and consequently the bacterial growth in sweet oranges (Muranaka et al., 2013).

Navarrete & De La Fuente (2015) studied the role of zinc in the growth and biofilm formation as well as in twitching motility of *X. fastidiosa* subsp. *fastidiosa* in tobacco plants. High levels of zinc can be deleterious to the growth of some microorganisms. In this study, the authors constructed two knockout mutants of *X. fastidiosa* (uptake regulation and influx). The increasing zinc concentrations in the mutants showed reduced leaf symptoms in two mutants when compared with the wild type as well as a reduction in twitching motility. This implies that zinc detoxification plays an important role in virulence of the pathogen and that the concentration of this metal in the plant plays a role in *X. fastidiosa* growth and symptoms. Although, so far, no practical treatment exists.

Also, the olive cultivar 'Leccino' shows noticeable resistance to *X. fastidiosa*, although the mechanism of this resistance is still unclear (Vergine et al., 2020). Vergine et al. (2020) performed a large-scale study of the olive tree microbiome, in an *Xylella*-resistant cultivar 'Leccino' and *Xylella*-susceptible cultivar 'Cellina di Nardò'. Their results highlighted that the endophytic bacterial microbiota in the leaves of the 'Leccino' cultivar appeared more stable and was more diverse, including cultivar-specific bacterial taxa that "appeared to interact, directly or indirectly, with *X. fastidiosa*". These results suggest that a healthy microbiota and the presence of cultivar-specific microbes might support the resistance of

the ‘Leccino’ cultivar to the phytopathogen and that their study and identification have possible potential for biological treatment for the OQDS.

Currently, the adopted strategy for olive orchards is establishing a containment belt, buffer zone and eradication area. In the first two areas mentioned, a continuous and extensive monitoring plan is established to survey for the presence of the phytopathogen by monitoring the health of the olive trees and alternative hosts, examining also for the presence of infective vectors; maintaining the health of olive trees by chemical control of vectors and mechanical weeding, and eliminating the alternative hosts from areas surrounding the culture. In the eradication area, vectors are to be submitted to chemical control and monitoring, identification, and elimination of infection foci (location, number and size) is to occur. Although this was only partially implemented in Italy due to opposition from environmentalists and grower associations as the olive trees are “majestic” and characterize the landscapes of Italy (Martelli, 2016).

1.9. National importance of olive culture

In the European Union, Portugal is one of the top four producers of olive oil, alongside Spain, Italy and Greece (EC, 2020). In 2019, Portugal broke a record of production of olives for olive oil, producing 943 thousand tons of olives, making the 2019 campaign as the most productive since 1941 (INE 2020a). With this record, there was an increase in olive oil production, exceeding, for the first time in the last 105 years, 1.5 million hectolitres (INE, 2020b). The Alentejo Region contributed significantly to these phenomena producing, in the last five years, on average more than 70% of the national production of olives for olive oil (INE 2020a).

In Alentejo Region, the main economic activities revolve not only around olive groves but also vineyards, cereal, fruit orchards, pastures and derived products, among others, representing a noticeable diversity, whether in demographic terms, as well as in terms of resources and their use.

1.10. Aim of this study

The significance of the olive culture in Portugal (particularly in Alentejo) and the devastating consequences of *X. fastidiosa* spread in Italian olive culture, highlight the contamination risk of this crop by the bacterium. Adequate management measures are dependent on the local knowledge of the phytopathogen vectors and their dynamics, making it imperative to study the occurrence of its vectors in olive orchards in this region.

Considering the above, the aim of this study was to survey the insect vectors of *X. fastidiosa* in Alentejo, in pesticide free olive orchards and contribute to a continuous monitoring plan of the vectors, thus preventing or limiting the occurrence of the OQDS.

To achieve this, the specific tasks were: i) identifying the presence and spread of potential vector species of *X. fastidiosa* in olive trees and in alternative hosts; ii) testing the presence of the bacterium in the captured vectors and iii) contributing to the development of an integrated control program of *X. fastidiosa* in olive orchards.

2. Material and Methods

2.1. Study area

2.1.1. General characterization

The Alentejo Region (centre-south of Portugal), where this study was conducted, occupies approximately 27323 km^2, corresponding to about 29% of the area of Portugal (Almeida et al., 2002). The dominant and characteristic land-use in the Alentejo Region is the Montado, an agro-silvo-pastoral system, characterized by the combination, in various densities, of an open tree cover of cork oak (*Quercus suber*) and holm oak (*Quercus rotundifolia*), with a rotation at the soil level, of cultures, grazing and fallow (Correia, 1993; 2000). The region is characterized by a dry summer Mediterranean climate (Csa) according to Koppen climate classification (https://www.ipma.pt/pt/educativa/tempo.clima).

2.1.2. Meteorological conditions

In order to characterize the meteorological conditions of the study area, data relative to the mensal minimum **(Annex A: Table A.1)**, mean **(Annex A: Table A.2)** and maximum **(Annex A: Table A.3)** temperatures (ºC) and total precipitation (mm) **(Annex A: Table A.4)** between January 2017 and December 2017 were obtained for 20 climatological stations spread nationally (**Annex A: Table A.5**) from Mensal Climatological Bulletins provided online (http://www.ipma.pt/pt/publicacoes/boletins.jsp?cmbDep=cli&cmbTema=pcl&cmbAno=2017&idDep=cli&idTema=pcl&curAno=2017) by Instituto Português do Mar e da Atmosfera (IPMA).

These data were used to calculate the monthly value of each climatic variable in the study region according with the Inverse Distance Weighting (IDW) method. This method is widely used and was chosen since temperature and precipitation are variables that usually do not vary abruptly in small regions (Noori et al., 2014) and that it is the method used by IPMA to produce the maps shown on the climatological bulletins. IDW interpolation of the four climatic variables was implemented with the *Interpolation* plugin in QGIS Desktop version 3.10, considering a $p = 2$ and a cell size of 1 km.

2.2. Arthropod sampling

The sampling period occurred between 3rd May and 8th June 2017 in the Alentejo Region, which was divided into 18 geographic units (GUs) of 30 × 30 km (**Annex B: Figure B. 1**) where seven traditional olive orchards, without insecticides' application, per GU were selected for prospection, resulting in a total of 126 sampling points (**Figure 2.1**). This allows a more homogenous distribution of sampling sites in the study area. Sampling sites' location (GPS coordinates) was recorded in WGS84 coordinate system. At each sampling point, arthropod fauna was captured in olive trees and surrounding ground vegetation using a John W. Hock Company gasoline-powered Agricultural Backpack 2-Cycle Aspirator Model 1612 with a 12.7 cm diameter collection nozzle and 64 km/h air intake.

In all sampling points, the all-around canopy of five olive trees was vacuum sampled for 50 s (10 s/ tree). In five sampling points per GU (**Figure 2.1**), the ground vegetation was vacuum sampled for 50 s, without plant species discrimination. In the remaining and randomly selected two sampling points of each GU (**Figure 2.1**), five of the most common plant species in the herbaceous vegetation were sampled individually (50 s/ plant species) and collected for posterior identification. The arthropod collection methodology was decided within the scope of the project "A protecção integrada do olival alentejano. Contributos para a sua inovação e melhoria contra os seus inimigos-chave" and was performed by the

external supervisor and collaborators. Plant species identification was performed by Prof. Anabela Belo, Departamento de Biologia, Instituto de Ciências Agrárias e Ambientais Mediterrânicas (ICAAM), Universidade de Évora. Collected samples were stored at -20°C until sorting and identification.

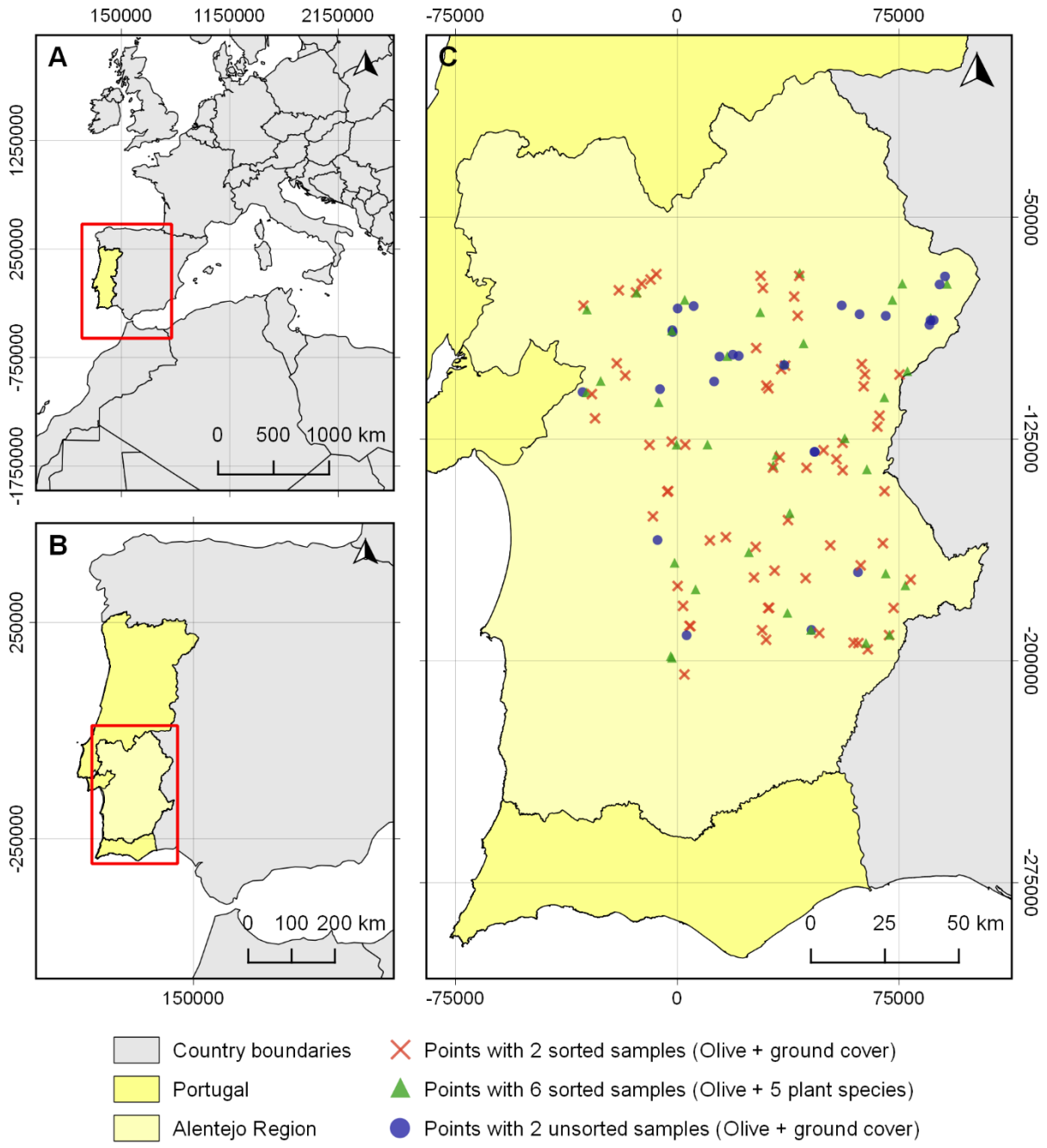

Figure 2.1 – Study area. **A** – Delimitation of location of Portugal in Europe. **B** – Delimitation of the Alentejo Region in Portugal. **C** – Sampling points in the Alentejo Region. Maps projected in ETRS89/TM06-PT.

2.3. Sorting and identification

2.3.1. Auchenorrhyncha identification

Collected samples were sorted to orders according to Chinery (1988) with the help of an Olympus SZX7 -TR30 stereomiscroscope. Individuals were counted, categorized and stored, according to their order, in labelled microtubes containing 70% ethanol.

Auchenorrhyncha adults were morphologically identified to species in Laboratório de Entomologia da Faculdade de Ciências da Universidade de Lisboa, according to the following literature: Bertin et al. (2010); Biedermann & Niedringhaus (2009); della Giustina (1989); Dietrich (2005); Dmitriev (2003-present); Drosopoulos & Quartau (2002); Drosopoulos & Remane (2000); Gnezdilov (2003, 2014); Holzinger (2008); Holzinger et al. (2003); Le Quesne (1965, 1969); Mozaffarian et al. (2018); Ribaut (1952); Rodrigues (1968); and Wilson *et al*. (2015). Studied specimens were deposited in the Laboratório de Entomologia do ICAAM, Universidade de Évora.

2.3.2. Genitalia preparation

Identification of Auchenorrhyncha often requires the dissection of the male genitalia. Auchenorrhyncha have eleven abdominal segments, in males the segments IX, X and XI are modified and correspond to the genital structures, while in females, the VIII segment is also part of the genital structures. Therefore, the abdomen should be dissected between segments VIII and IX, but a more anterior dissection is advisable when there is lack of experience to avoid damaging the genital structures. The last abdominal segments were detached from each specimen with a sterile dissection needle and tweezers, under observation with an Olympus SZX7-TR30 stereomicroscope. The dissected abdomen was placed in a boiling solution of 10% (w/v) Potassium Hydroxide (KOH) from 20 s to 2 min and transferred into a drop of pharmaceutical glycerine on a glass slide for removal of unwanted tissues and cleaning of the genital structures. Immersion time in KOH solution varied proportionally to the degree of sclerotization of each specimen. Cleared genitalia was then mounted into a new drop of pharmaceutical glycerine on glass slides, sealed with nail polish and observed under a Nikon XSZ-107BN binocular optical microscope for identification.

Female genitalia are highly preserved among Auchenorrhyncha, being less morphologically variable than male genitalia at the genus or species level. For this reason, most identification literature is based on male genitalia. However, recent studies focused on the morphological diversity of female genitalia show potential taxonomic interest of some features of female genitalia in some groups within Auchenorrhyncha (Carvalho & Mejdalani, 2014; Demichelis et al. 2010; Gnezdilov, 2003).

The females were identified to the lowest taxonomic unit possible. When all males from a certain genus belonged exclusively to one species in a distinct sample, females from the same genus in the same sample were attributed the same species as males, after it was determined that they shared identical morphological characters.

When species identification was not possible, morphospecies designated by the respective genus, tribe or subfamily followed by “sp.”, and a number corresponding to the morphotype were considered.

2.3.3. Image acquisition and processing

Specific identification of Auchenorrhyncha often requires preparation of the male genitalia which implies partial destruction of the specimens, thus a photographic record of the external morphology of a representative specimen of each species/ morphospecies was compiled (one male and one female, whenever possible) prior to specimen dissection. Pictures from genital structures for each species/ morphospecies were also taken when available.

Images were acquired on a Zeiss Stereo Lumar V.12 stereomicroscope, equipped with a Zeiss Axiocam 503 colour camera, controlled with AxioVision 4.9.1 64 bit software. Multiple images acquired at different focus distances were combined via focus stacking with the help of the tool “Extended Focus” from AxioVision, using the Wavelets method.

Images of male genitalia were acquired using an Olympus BX51 microscope, equipped with a The Imaging Source DFK 23U274 colour industrial camera controlled with MicroManager 2.4 software. Some images were acquired as z-stacks and processed with the plugin "Extended Depth of Field" (Forster et al., 2004) in ImageJ, using the Wavelets methods. All images were processed and scaled in ImageJ 1.52n.

2.4. Molecular detection of *Xylella fastidiosa* in potential vectors

2.4.1. Preparation of samples from specimens

Potential vectors of *X. fastidiosa* were tested for the presence of the bacterium. Since this bacterium colonizes exclusively the foregut of its insect vectors and is non-circulative, only the insect head was used to detect the presence of *X. fastidiosa*, thus "avoiding the extraction of several contaminants that may inhibit Taq Polimerase-dependent amplification" (Morelli, 2014). Each specimen was placed under an Olympus SZX7-TR30 stereomicroscope, the body rotated sideways, and the head was separated from the body by gently pressing a scalpel, in a diagonal direction, between the vertex and the pronotum. Afterwards, given a previous recommendation from EPPO (2016), the eyes were also removed, as it was reported they could affect the sensitivity of Quantitative Polymerase Chain Reaction (qPCR) detection. However, a more recent inter-laboratory report showed no difference in qPCR detection sensitivity between vectors with and without eyes (Legendre et al., 2018). After this, one to five insect heads per species or genus were pooled by sampling point, irrespective of plant host. Each pool was placed in a microtube of 1.5 mL containing ethanol (96%) and transported to Laboratório de Virologia Vegetal, Universidade de Évora where the molecular detection tests of the bacterium were performed.

2.4.2. DNA extraction

Before proceeding with DNA extraction, it is important to remove the ethanol since it penetrates in the insect tissues and could interfere with molecular analysis. All heads were washed twice in ultrapure water (type 1). For this, each head was dried with a filter paper, then placed, for a few seconds, in a glass cup, matching its pool, filled with ultrapure water (type 1), to remove the excess of ethanol. After, the heads were dried with filter paper, the water changed, and the heads placed once more in the ultrapure water (type 1) for 30 min to eliminate the ethanol from the tissue. Each pool was then transferred to a microtube of 2 mL since the micropestles used for maceration of the heads of the vectors were too broad to reach the bottom of 1.5 mL microtubes. The microtubes of each pool were stored, for at least 12 h, at -20 ºC, to preserve DNA and to facilitate maceration.

After sample maceration, the DNA extraction was performed using the Cetyl Trimethyl Ammonium Bromide (CTAB) method (Doyle & Doyle, 1987) with some modifications as described by Varanda et al. (2016). DNA concentration was determined with a Quawell Q9000 spectrophotometer (Quawell Technology, USA).

2.4.3. Quantitative Polymerase Chain Reaction

Subsequently to DNA extraction, the Taqman version of qPCR was performed to test the presence of *X. fastidiosa*, following the methodology described by Campos et al. (2019). The primers and probe used in this study were the same as described by Francis et al. (2006), namely the primer pair HL5 forward (5'-AAGGCAATAAACGCGCACTA-3'), HL6 reverse (5'-GGTTTTGCTGACTGGCAACA-3') and the probe sequence (5'/FAM/-TGGCAGGCAGCAACGATACGGCT-/BHQ1/3'). qPCR was carried

with 10 µL of TaqMan Universal PCR Master Mix, 0.8 µL of each primer, 0.2 µL of probe sequence, 5.2 µL of H_2O and 3 µL of gDNA, per sample, in a total volume of 20 µg/ µL.

Three technical replicates were considered for each sample. *Xylella fastidiosa*-positive target controls and no template controls were included in all plates. The fluorescence threshold was manually set to 0.05, since it is when the amplification of *X. fastidiosa* DNA begins in the positive controls. Cycling conditions of qPCR were the following: 5 min at 94 °C for initial denaturation, an amplification program of 35 cycles composed by denaturation at 94 °C for 20 s, annealing at 50 °C for 30 s and extension for 50 s at 72 °C, finishing with a final extension at 72 °C for 7 min and a resting phase at 10 °C. Quantification cycle (Cq) values were acquired for each sample with the Applied Biosystems 7500 software v2.0.6 (Applied Biosystems, Foster City, CA, USA).

2.5. Data analysis

Collected Auchenorrhyncha were categorized, as described by Tsagkarakis et al. (2018), by criteria of dominance (percentage of individuals of each taxon, among the total number of individuals of all taxa found) and frequency (percentage of each species relative to the total number of individuals collected). A taxon is classified as 'dominant', 'influent' or 'recedent', if it constitutes >10, 5-10 or <5% of the total number of individuals, respectively. Similarly, three categories are also defined for frequency, specifically 'constant', 'accessory' or 'accidental', if a species occurs in >50, 25-50 or <25% of the total number of samples, respectively.

The effect of 22 independent variables (**Table 2.1**) on the abundance of species of *X. fastidiosa* vectors. A non-parametric analysis of variance (Kruskal-Wallis test) was performed to identify statistically significant differences among classes of these variables, when significant differences were identified, the variable data were ranked and subsequently discriminated by the *post hoc* least significant difference (LSD) test, as described by Marôco (2007).

Two datasets were used for the analysis of the effect of different factors on species abundance. A dataset composed exclusively of samples of individual spontaneous plant species was used for the analysis of "Plant family", "Plant genus" and "Plant species" effect on the abundance of relevant insect species. The second dataset with samples from olive trees and mixed ground cover was used to evaluate the effect of the remaining 19 tested factors. Samples of mixed ground cover were considered in this dataset by aggregating captures from five individual plant species of the same sampling point.

In this dissertation, all maps were elaborated in QGIS. The metadata associated with the data used in this study can be found in **Annex C: Table C.1**. Data related with soil occupation (i.e. Olivdist, Oliv250, Oliv500, Oliv1000, Ripdist, Rip250, Rip500, Rip1000, Vine250, Past250, Holm250 and Cork250) were provided by Dr. Luís Alexandre Piteira Gomes (ICAAM).

Table 2.1 - Independent variables tested in this study with respective name, code (an abbreviation for the variable name), unit and class.

Variable name	Code	Unit	Class
Geographic unit	GU	-	See **Annex B - Figure B. 1**
Host plant	Host	-	Olive Mixed ground cover
Plant family	Fam	-	See **Table 3.4**
Plant genus	Gen	-	See **Table 3.5**
Plant species	Spe	-	See **Table 3.6**

Table 2.1 (cont.) - Independent variables tested in this study with respective name, code (an abbreviation for the variable name), unit and class.

Variable name	Code	Unit	Class
Distance to water	DistWat	m	[0, 100]]100, 500]]500, 1000]]1000, 2000] > 2000
Altitude	Alti	m	[0, 50]]50, 100]]100, 200]]200, 300] > 300
Aspect	Asp	º	North: [0, 45] ∪]316, 360] East:]45, 135] South:]135, 225] West:]225, 315]
Mean temperature	Tmed	ºC	19 21 24 26 28
Total precipitation	Prec	mm	5 10 25 50
Distance to olive groves	OlivDist	m	[0, 50]]50, 100]]100, 250]]250, 1000] > 1000
Area of olive groves in 250 m radius	Oliv250	%	0]0, 25]]25, 50]]50, 75]]75, 100[100
Area of olive groves in 500 m radius	Oliv500	%	0]0, 25]]25, 50]]50, 75]]75, 100[100
Area of olive groves in 1000 m radius	Oliv1000	%	0]0, 25]]25, 50]]50, 75]]75, 100[100
Distance to riparian zones	RipDist	m	[0, 50]]50, 100]]100, 250]]250, 1000] > 1000

Table 2.1 (cont.) - Independent variables tested in this study with respective name, code (an abbreviation for the variable name), unit and class.

Variable name	Code	Unit	Class
Area of riparian zones in 250 m radius	Rip250	%	0]0, 25]]25, 50]]50, 75]]75, 100[100
Area of riparian zones in 500 m radius	Rip500	%	0]0, 25]]25, 50]]50, 75]]75, 100[100
Area of riparian zones in 1000 m radius	Rip1000	%	0]0, 25]]25, 50]]50, 75]]75, 100[100
Area of vineyards in 250 m radius	Vine250	%	0]0, 25]]25, 50]]50, 75]]75, 100[100
Area of pastures in 250 m radius	Past250	%	0]0, 25]]25, 50]]50, 75]]75, 100[100
Area of holm oak in 250 m radius	Holm250	%	0]0 25]]25, 50]]50, 75]]75, 100[100
Area of cork oak in 250 m radius	Cork250	%	0]0, 25]]25, 50]]50, 75]]75, 100[100

3. Results

3.1. Meteorological conditions

In 2017, the hottest month was August, with an average maximum, mean and minimum temperature of 32.4 ºC, 24.1 ºC and 15.9 ºC, respectively. January was the coldest month with the average maximum, mean and minimum temperature of 13.5 ºC, 8.7 ºC and 3.9 ºC, correspondingly. During the sampling period, the average maximum, mean and minimum temperatures in the months of May and June were 25.7 ºC, 19.1 ºC and 12.4 ºC; and 31.7 ºC, 23.3 ºC and 15.7 ºC, respectively. During 2017, the wettest month was March with an average precipitation of 76.4 mm, whereas the driest months of the year were September and July, with 0.3 mm and 0.9 mm, respectively. During the sampling period, May was the wettest month with an average precipitation of 46.7 mm and June was the driest month with only 5.7 mm (**Figure 3.1**).

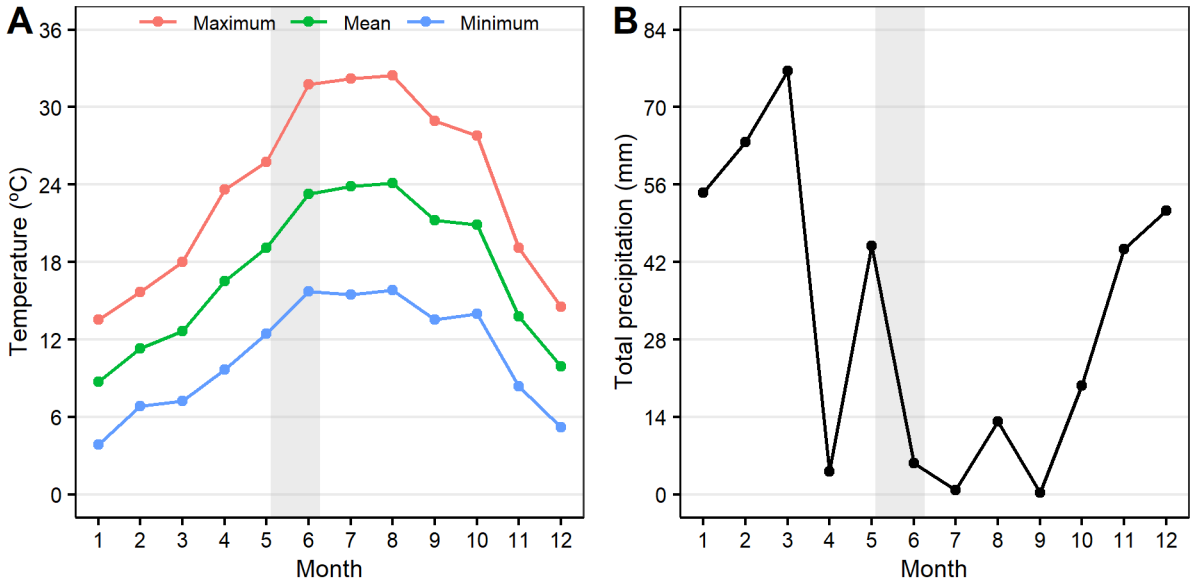

Figure 3.1 – Average values of meteorological variables in the sampling points during 2017. **A** – Temperature (ºC) (maximum, mean and minimum) and **B** – total precipitation (mm). The gray rectangle indicates the sample period.

3.2. Terrestrial invertebrates' abundance and diversity

From 300 samples collected in the Alentejo Region, 99 were from olive trees, 21 from mixed ground vegetation and 180 from individual plant species**.** In total 39 527 arthropods where collected (including adults and immatures), belonging to 20 orders, namely: Acari, Aranea, Blatodea, Coleoptera, Collembola, Dermaptera, Diptera, Hemiptera, Hymenoptera, Lepidoptera, Mantodea, Mecoptera, Neuroptera, Orthoptera, Phasmatodea, Pscocoptera, Pulmonata, Raphidioptera, Thysanoptera and Thysanura. The most abundant taxon was Hemiptera, which corresponded to 28% of collected specimens, followed by Thysanoptera, Hymenoptera and Acari, each with approximately 13% of the collected specimens (**Table 3.1**).

3.3. Auchenorrhyncha abundance and diversity

Overall, 11 022 Hemiptera individuals (**Table 3.1**) were collected, out of which 1 145 were Auchenorrhyncha, corresponding to approximately 10% of collected Hemiptera, including adults and immature stages. From all Auchenorrhyncha, 954 individuals were from the infra-order Cicadomorpha,

of which 224 were nymphs and 730 adults. From these adults, 297 were female, 380 male and 53 could not have the sex determined, due to the missing abdomen. The remaining 191 Auchenorrhyncha belonged to the infra-order Fulgoromorpha, of which 92 were nymphs and 99 adults (33 females and 66 males).

Table 3.1 – Total abundance of collected individuals by order and sample type.

Ordem	Olive	Mixed ground cover	Individual plant species	Total
Acari	121	443	4 638	5 202
Aranea	739	354	922	2 015
Blatodea	0	0	8	8
Coleoptera	743	292	2 234	3 269
Collembola	1	3 218	90	3 309
Dermaptera	33	0	1	34
Diptera	1 196	381	1 318	2 895
Hemiptera	4 793	1 000	5 229	11 022
Hymenoptera	1 787	667	2 773	5 227
Lepidoptera	80	21	63	164
Mantodea	4	1	2	7
Mecoptera	1	0	0	1
Neuroptera	140	8	25	173
Orthoptera	10	75	94	179
Phasmatodea	0	1	1	2
Pscocoptera	462	5	6	473
Pulmonata	22	43	201	266
Raphidioptera	1	0	0	1
Thysanoptera	784	492	4 003	5 279
Thysanura	0	1	0	1

A total of 811 out of 829 Auchenorrhyncha adults were identified to 61 species/ morphospecies, belonging to 8 families. The richest family in species diversity was Cicadellidae, with 41 species, corresponding to approximately 66% of identified species. Dominance rankings revealed one dominant species, *Zyginidia scutellaris* (Herrich-Shäffer), and two influent species: *Philaenus tesselatus* Melichar and *Empoasca solani* (Curtis). The remaining species were classified as recedent, having less than 5% dominance. In terms of frequency all species were defined as accidental, with only *Z. scutellaris* being considered as an accessory species (**Table 3.2**).

Habitus from 32 of collected Auchenorrhyncha species/ morphospecies and genitalia of 26 species/ morphospecies are shown in **Annex D**. Highlighting that from 1 145 Auchenorrhyncha, 11 individuals were parasitized: five adults belonging to *Empoasca solani* (Curtis), *Lindbergina aurovittata* (Douglas), *Metadelphax propinqua* (Fieber), *Euscelis alsius* Ribaut and *Euscelis distinguendus* Kirschbaum; plus six nymphs, half from Cicadomorpha and half from Fulgoromorpha. All parasitized specimens, except for *E. distinguendus* were parasitized by Dryinidae (Hymenoptera: Chrysidoidea), the other parasitoid could not be identified. Interestingly, two individuals belonging to *Arocephalus punctum* (Flor) were found in this study.

Table 3.2 - Total number (N), dominance (D) and frequency (F) of Auchenorrhyncha species collected in Alentejo Region during spring of 2017 (3 of May to 8 of June).

Infra-order	Family	Subfamily	Species	N	D (%)	F (%)
Cicadomorpha	Aphrophoridae	Aphrophorinae	*Lepyronia coleoptrata* (Linnaeus)	4	0.49	0.67
			Neophilaenus campestris (Fallén)	5	0.62	1.67
			Philaenus sp.	13	1.60	4.00
			Philaenus spumarius (Linnaeus)	1	0.12	0.33
			Philaenus tesselatus Melichar	57	7.03	13.33
	Cercopidae	Cercopinae	*Cercopis intermedia* Kirschbaum	1	0.12	0.33

Table 3.2 (cont.) – Total number (N), dominance (D) and frequency (F) of Auchenorrhyncha species collected in Alentejo Region during spring of 2017 (3 of May to 8 of June).

Infra-order	Family	Subfamily	Species	N	D (%)	F (%)
Cicadomorpha (cont.)	Cicadellidae	Agalliinae	*Agallia consobrina* Curtis	7	0.86	1.67
			Agallia sp1	3	0.37	1.00
			Agallia sp2	2	0.25	0.67
			Anaceratagallia laevis (Ribaut)	15	1.85	4.33
			Anaceratagallia sp.	1	0.12	0.33
			Austroagallia sinuata (Mulsant & Rey)	29	3.58	6.00
		Deltocephalinae	*Allygus provincialis* (Ferrari)	32	3.95	6.33
			Anoplotettix ibericus Remane	1	0.12	0.33
			Arocephalus punctum (Flor)	2	0.25	0.67
			Athysanini sp1	2	0.25	0.67
			Athysanini sp2	1	0.12	0.33
			Athysanini sp3	1	0.12	0.33
			Athysanini sp4	1	0.12	0.33
			Deltocephalinae sp1	1	0.12	0.33
			Deltocephalinae sp2	1	0.12	0.33
			Eupelix cuspidata (Fabricius)	1	0.12	0.33
			Euscelidius variegatus (Kirschbaum)	8	0.99	2.33
			Euscelis alsius Ribaut	18	2.22	4.33
			Euscelis distinguendus Kirschbaum	14	1.73	3.33
			Goniagnathus brevis (Herrich-Schäffer)	5	0.62	0.67
			Goniagnathus guttulinervis (Kirschbaum)	2	0.25	0.67
			Macrosteles sp.	1	0.12	0.33
			Neoaliturus fenestratus (Herrich-Shäffer)	2	0.25	0.33
			Oxytettigella viridinervis (Kirschbaum)	2	0.25	0.67
			Phlepsius spinulosus Wagner	1	0.12	0.33
			Psammotettix sp1	2	0.25	0.67
			Psammotettix sp2	1	0.12	0.33
			Psammotettix sp3	2	0.25	0.67
			Psammotettix sp4	2	0.25	0.67
			Psammotettix sp5	1	0.12	0.33
			Selenocephalus conspersus (Herrich-Schäffer)	3	0.37	1.00
			Stegelytra putoni Mulsant & Rey	1	0.12	0.33
		Typhlocybinae	*Alnetoidia alneti* (Dahlbom)	1	0.12	0.33
			Empoasca decipiens Paoli	9	1.11	1.33
			Empoasca solani (Curtis)	41	5.06	6.00
			Eupteryx sp1	1	0.12	0.33
			Eupteryx sp2	1	0.12	0.33
			Lindbergina aurovittata (Douglas)	1	0.12	0.33
			Typhlocybinae sp1	1	0.12	0.33
			Zyginidia scutellaris (Herrich-Schäffer)	410	50.55	27.00
		Ulopinae	*Utecha trivia* (Germar)	1	0.12	0.33
Fulgoromorpha	Achilidae	Achilinae	*Cixidia* sp.	1	0.12	0.33
	Cixiidae	Cixiinae	*Hyalesthes luteipes* Fieber	6	0.74	1.67
			Hyalesthes obsoletus Signoret	11	1.36	2.00
			Hyalesthes sp.	8	0.99	1.33
	Delphacidae	Asiracinae	*Asiraca clavicornis* (Fabricius)	1	0.12	0.33
		Delphacinae	*Laodelphax striatella* (Fallén)	4	0.49	1.00
			Metadelphax propinqua (Fieber)	15	1.85	1.67
	Issidae	Issinae	*Agalmatium bilobum* (Fieber)	9	1.11	2.67
			Agalmatium flavescens (Olivier)	13	1.60	3.33
			Agalmatium sp.	9	1.11	2.67
			Palmallorcus punctulatus (Rambur)	5	0.62	1.67
	Tettigometridae	Tettigometrinae	*Tettigometra costulata* Fieber	5	0.62	1.33
			Tettigometra impressifrons Mulsant & Rey	2	0.25	0.33
			Tettigometra obliqua Panzer	10	1.23	2.33

3.4. Vector abundance and diversity

In this study, a total of 81 individuals belonging to five species of two distinct families (Cercopidae and Aphrophoridae) were considered as *X. fastidiosa* vectors or potential vectors, specifically: *Cercopis intermedia* Kirschbaum (**Figure 3.2**), *Lepyronia coleoptrata* (Linnaeus) (**Figure 3.3**), *Neophilaenus campestris* (Fallén) (**Figure 3.4**), *Philaenus spumarius* (Linnaeus) and *Philaenus tesselatus* Melichar (**Figure 3.5**). Male genitalia of collected vectors and potential vectors can be found in **Figure 3.6**.

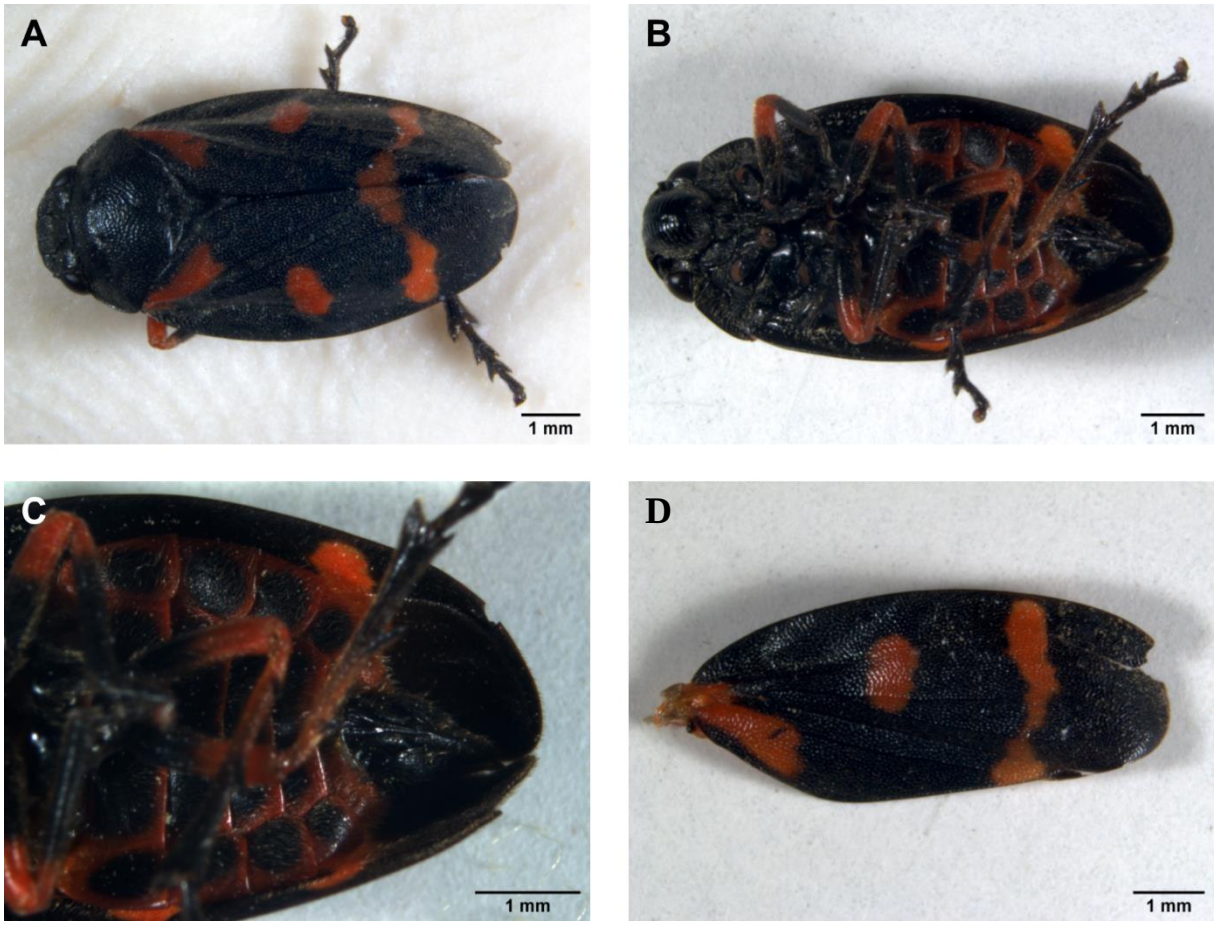

Figure 3.2 – External morphology of female *Cercopis intermedia* Kirschbaum. **A** –Dorsal view. **B** – Ventral view. **C** – Detail of genitalia in ventral view. **D** – Forewing.

The most dominant and frequent species among *X. fastidiosa* vectors/potential vectors was *P. tesselatus* (**Table 3.2**). On the other side, only one *P. spumarius* male and one *C. intermedia* female were found in this study. *Philaenus tesselatus* was the vector species most widely spread in the Alentejo Region, while *P. spumarius* distribution was limited to the northwest of the study area. *Cercopis intermedia* was found to be restricted to the south and *L. coleoptrata* occurred only in the east part of the region (**Figure 3.7**).

Philaenus spp. adults are polymorphic for the dorsal colour pattern (Weaver and King, 1954) and display great variation, with *P. spumarius* having at least sixteen naturally occurring phenotypes (Yurtsever, 2000). In this study, six different morphotypes were found, three of them non-melanic, essentially very pale brown with dark patterns - *populi* (POP), *typicus* (TYP) and *trilineatus* (TRI), two melanic forms, dark brown with various pale marking in the vertex, pronotum and wing patterns - *marginellus* (MAR) and *flavicollis* (FLA) and one rare phenotype, a combination of the two melanic forms - *marginellus*/*flavicollis* (MAR/FLA). The most abundant phenotypes found in this study, were non melanic, more specifically POP, which was present in approximately 66% of all *Philaenus* and TYP, in

approximately 24%. The only male individual of *P. spumarius* presented the TYP morphotype. The morphotypes where classified according to Yurtsever (2000) (**Table 3.3**).

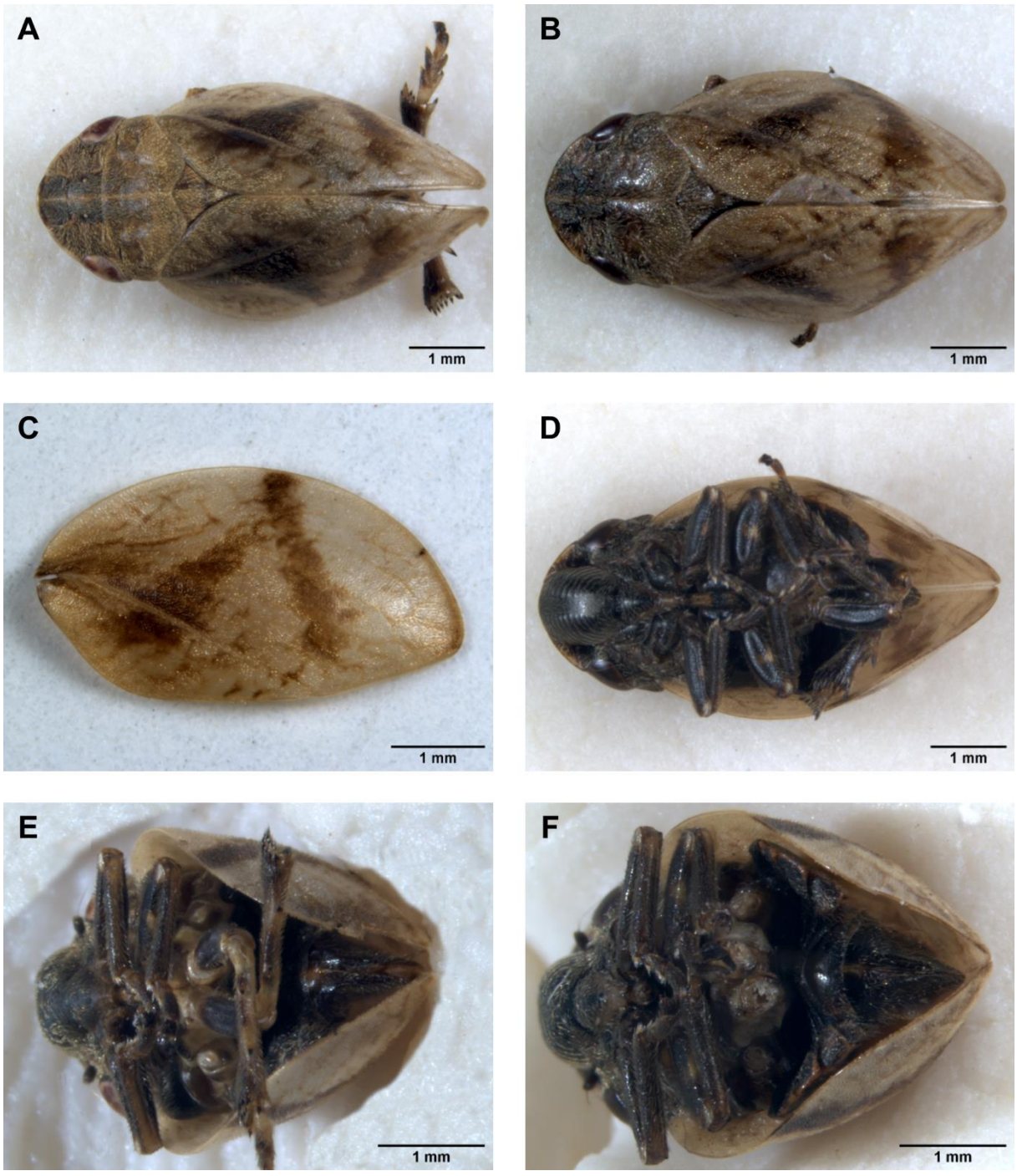

Figure 3.3 – External morphology of *Lepyronia coleoptrata* (Linnaeus). **A** – Male in dorsal view. **B** – Female in dorsal view. **C** –Male forewing. **D** – Female in ventral view. **E** – Detail of male genitalia in ventral view. **F** – Detail of female genitalia in ventral view.

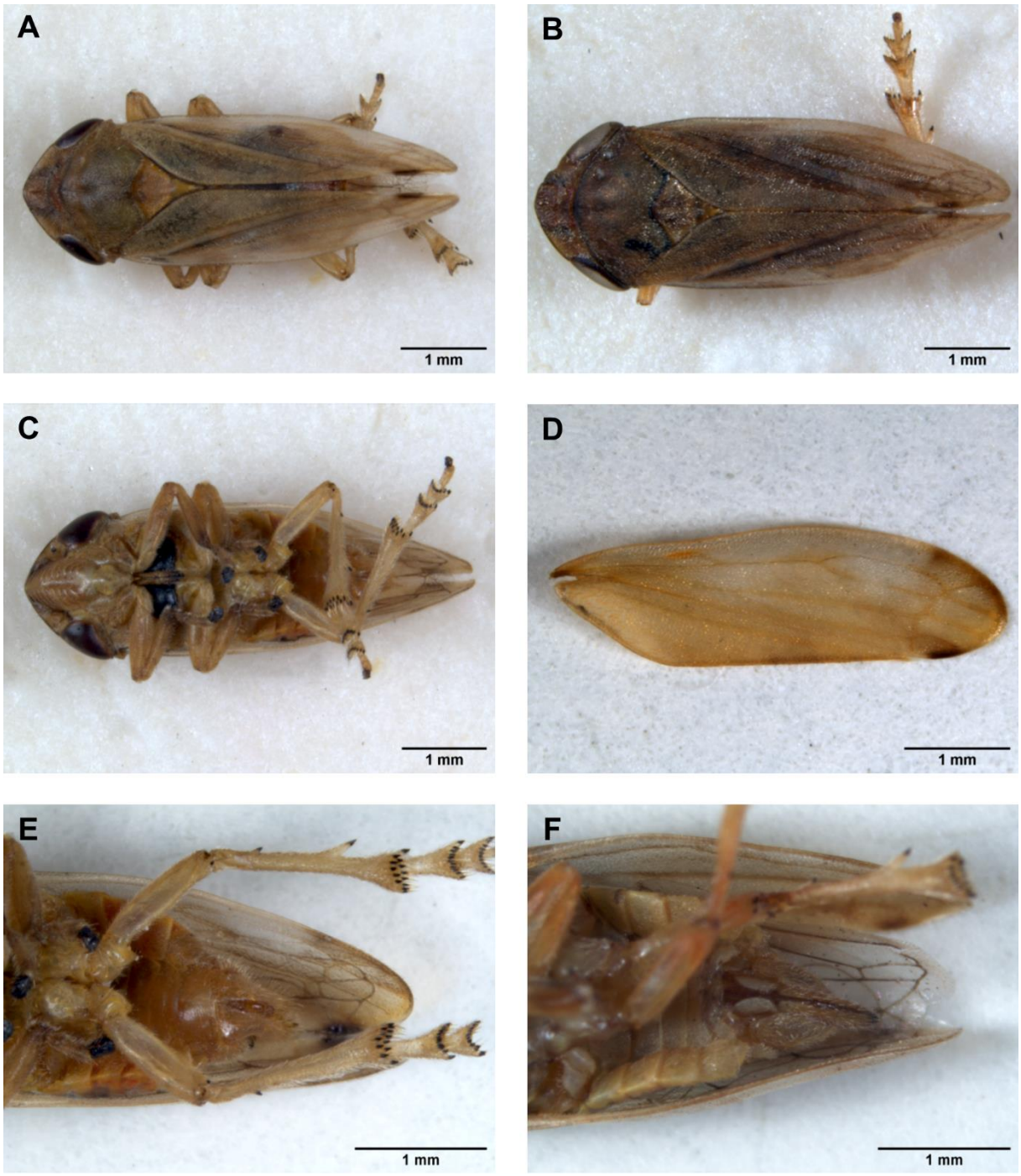

Figure 3.4 – External morphology of *Neophilaenus campestris* (Fallén). **A** – Male in dorsal view. **B** – Female in dorsal view. **C** – Male in ventral view. **D** – Male forewing. **E** – Detail of male genitalia in ventral view. **F** – Detail of female genitalia in ventral view.

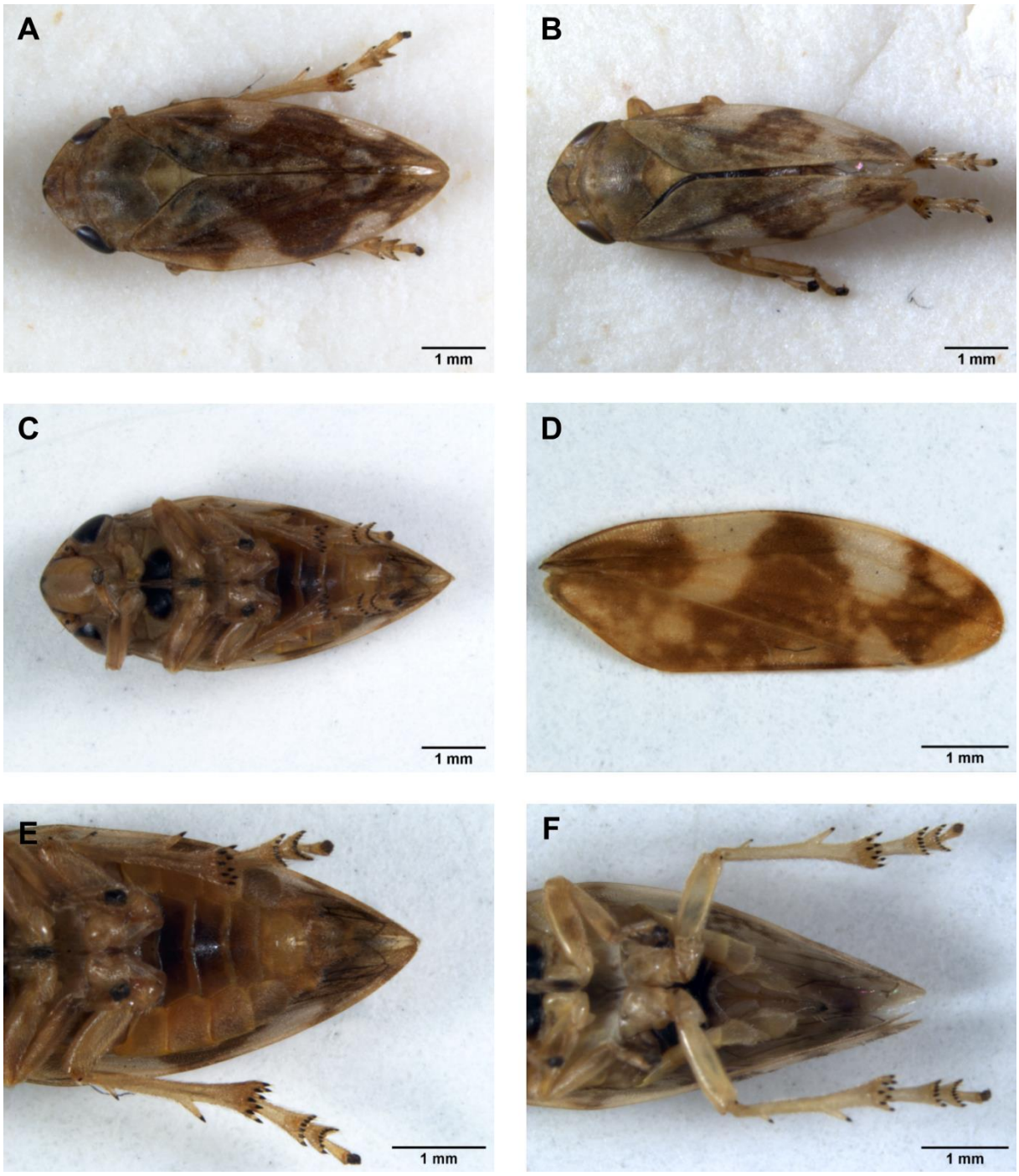

Figure 3.5 – External morphology of collected *Philaenus* spp. **A** – *Philaenus tesselatus* Melichar, male in dorsal view. **B** – *Philaenus spumarius* (Linnaeus), male in dorsal view. **C** – *P. tesselatus*, male in ventral view. **D** – *P. tesselatus* forewing. **E** – *P. tesselatus* detail of male genitalia in ventral view. **F** – Detail of female genitalia in ventral view.

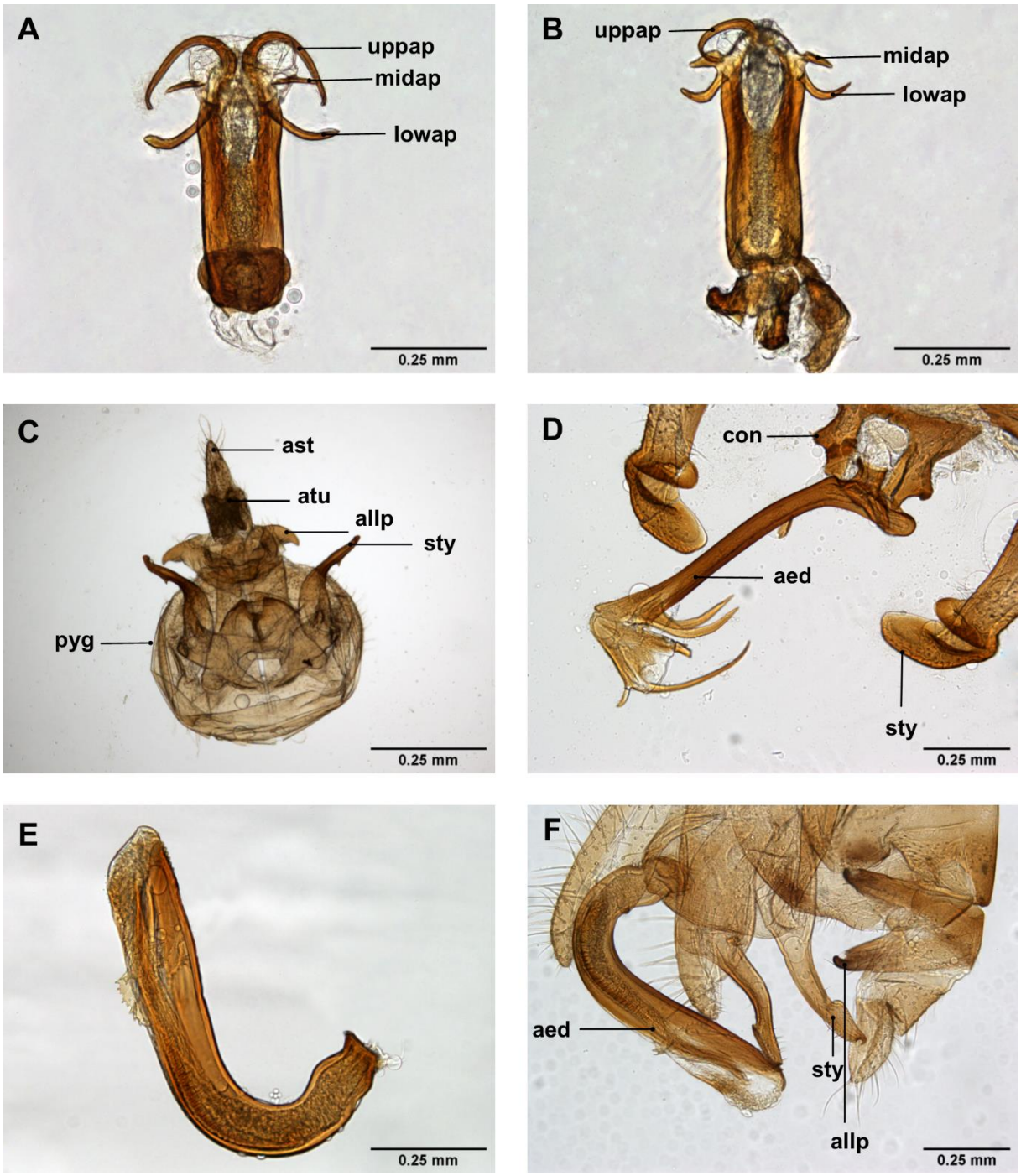

Figure 3.6 – Morphologic aspects of the male genitalia of four spittlebugs species. **A** – Aedeagus of *Philaenus tesselatus* Melichar. **B** – Aedeagus of *Philaenus spumarius* (Linnaeus). **C** – Genitalia of *P. tesselatus*. **D** – Genitalia of *Lepyronia coleoptrata* (Linnaeus). **E** – Aedeagus of *Neophilaenus campestris* (Fallén). **F** – Genitalia of *N. campestris*. aed = aedeagus; allp = appendages of lateral lobe of pygofer; ast = anal style; atu = anal tube; con = connective; lowap = lower appendages of aedeagus; midap = middle appendages of aedeagus; pyg = pygofer; sty = styles; uppap = upper appendages of aedeagus.

Table 3.3 - Dorsal colour morphotypes of the collected *Philaenus* spp. classified according to Yurtsever (2000). POP = *populi*, TYP = *typicus*, MAR = *marginellus*, FLA = *flavicollis*, MAR/FLA = *marginellus*/*flavicollis*, TRI = *trilineatus*.

Morphotype / Species	Non Melanic			Melanic		
	POP	TYP	TRI	MAR	FLA	MAR/FLA
						
P. spumarius	-	1♂	-	-	-	-
P. tesselatus	23♀; 15♂♂	4♀♀; 8♂♂	1♀; 1♂	1♀; 1♂	-	1♀; 2♂♂
Philaenus sp.	6♀♀	4♀♀	2♀♀	-	1♀	-
Total	**44**	**17**	**4**	**2**	**1**	**3**

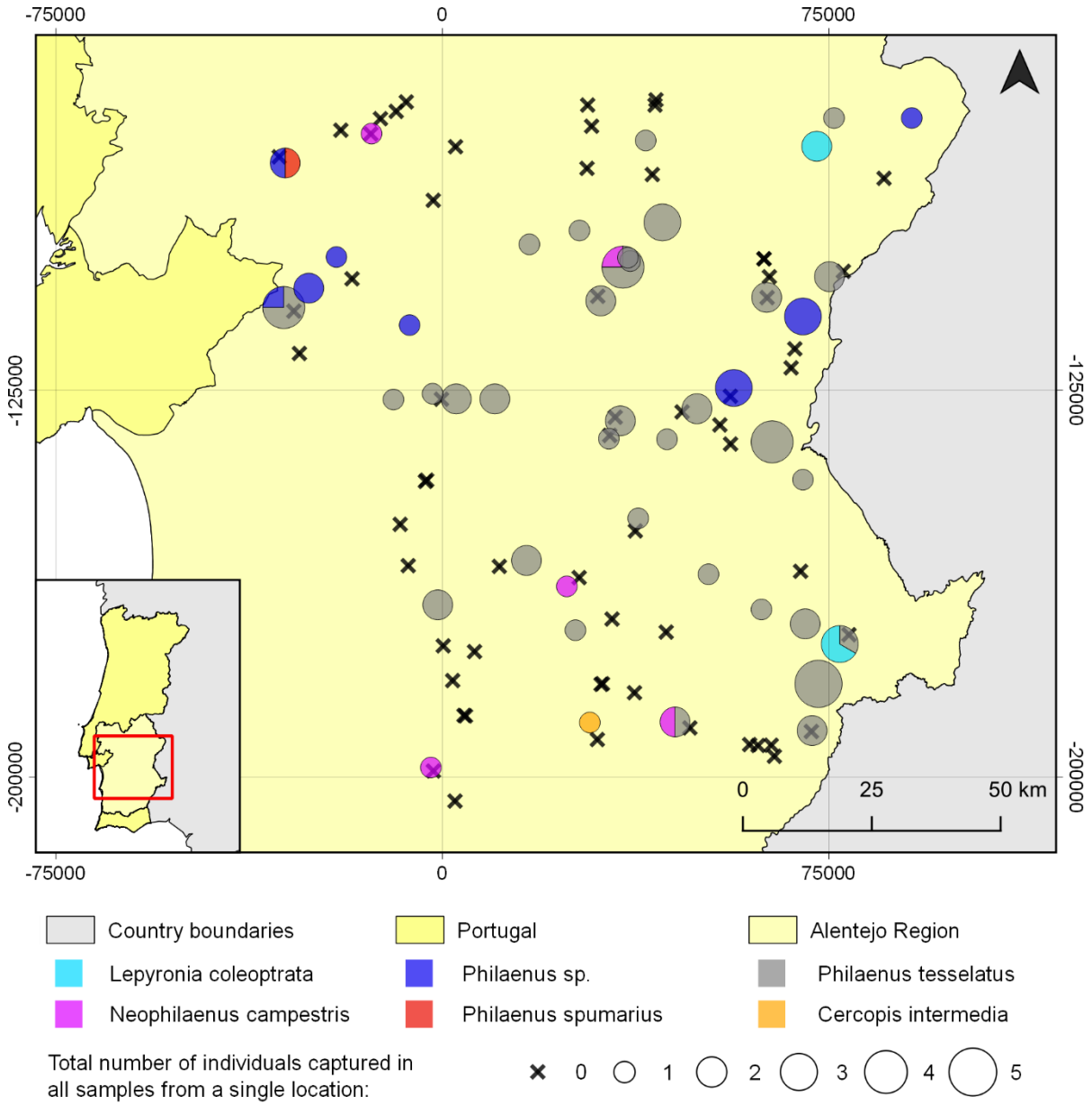

Figure 3.7 – Distribution of *Xylella fastidiosa* vector species in the Alentejo Region, as well as the number of individuals captured per species, in all samples per location. The number of collected specimens, per each location, is directly proportional to the size of the circles**.**

3.5. Detection of *Xylella fastidiosa* in vector species

Eighty-one individuals belonging to five vector species (*C. intermedia, L. coleoptrata, N. campestris, P. spumarius* and *P. tesselatus*) where tested for the presence of *X. fastidiosa*, in 42 pools (**Annex E: Table E.1**)**.** All pools tested in this study were negative for the presence of *X. fastidiosa*. The Cq of the positive control used in this assay was in the range of 12 to 13, presenting an exponential curve. No such curve was detected in the negative control, as well as in all 39 pools tested (**Figure 3.8A-B**). In **Figure 3.8C**, an exponential curve can be observed for some pools replicates, however, despite the amplification observed, the curve is below the defined threshold and the Cq is significatively higher than the positive control, which means these replicates were negative for the presence of the phytopathogen.

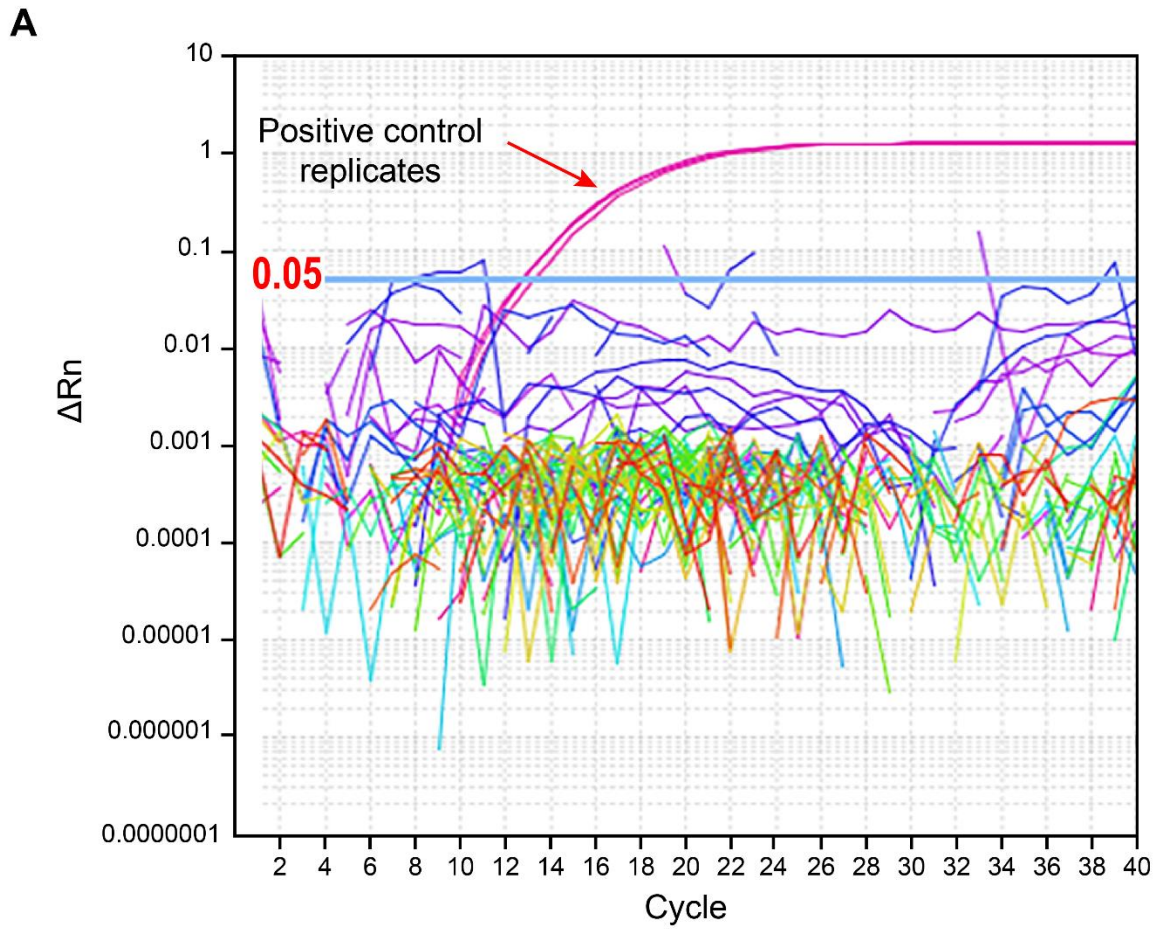

Figure 3.8 – qPCR amplification plots for *Xylella fastidiosa* detection. **A** – Pools 1 to 28. **B** – Pools 29 to 39. **C** – Pools 40 to 42. Horizontal blue line at ΔRn = 0.05 represents the manually set fluorescence threshold for positive detection. The exponential curves indicated with a red arrow represent the positive control replicates. All tested pools were below the 0.05 threshold and therefore considered negative for *Xylella fastidiosa*.

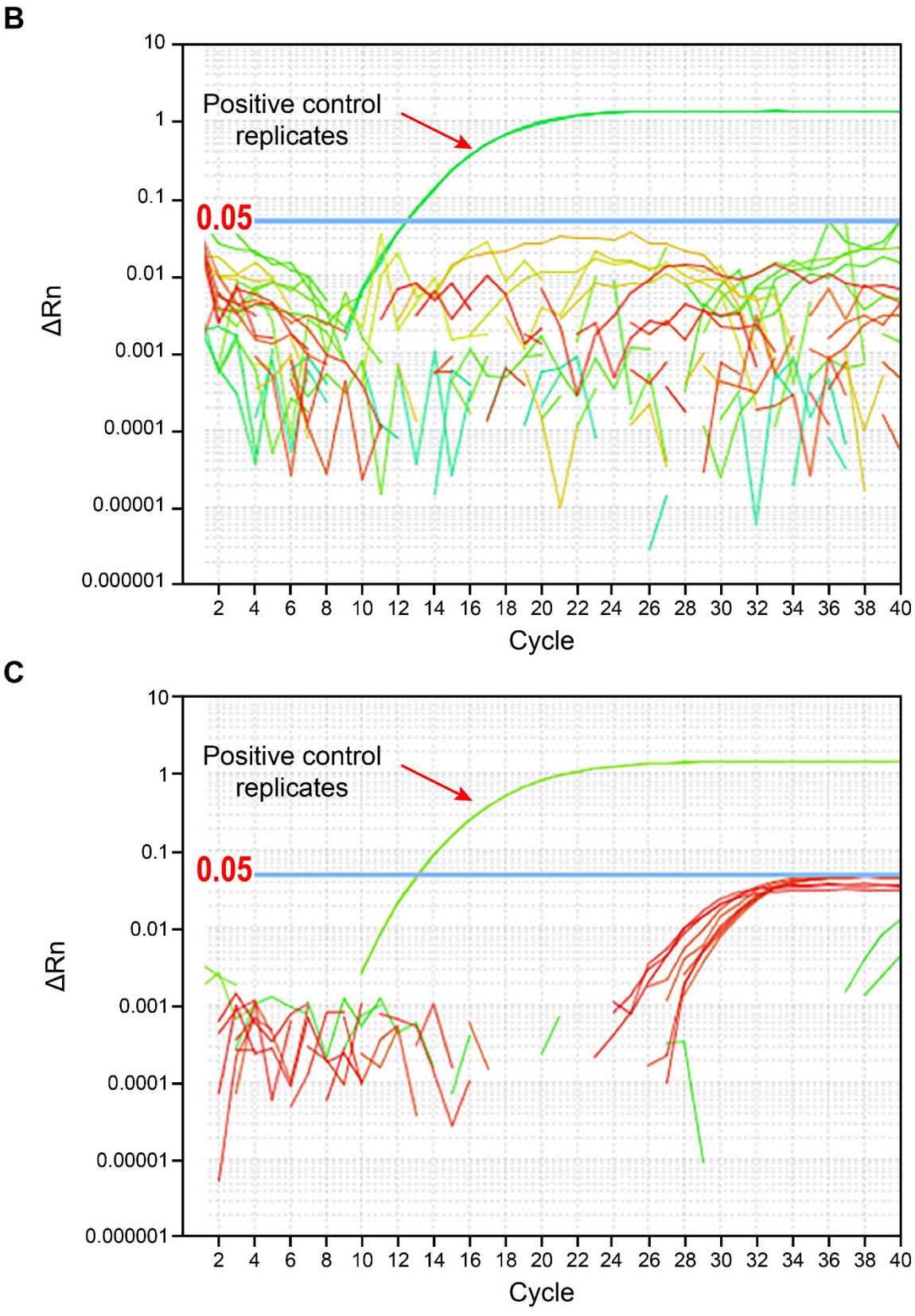

Figure 3.8 (cont.) – qPCR amplification plots for *Xylella fastidiosa* detection. **A** – Pools 1 to 28. **B** – Pools 29 to 39. **C** – Pools 40 to 42. Horizontal blue line at ΔRn = 0.05 represents the manually set fluorescence threshold for positive detection. The exponential curves indicated with a red arrow represent the positive control replicates. All tested pools were below the 0.05 threshold and therefore considered negative for *Xylella fastidiosa*.

3.6. Plant species/vector relation

From the 300 sorted samples, 6 were excluded from the analysis of the following results due to incomplete information about the sample prior to sorting. A total of 57 individual plant species belonging to 45 genera of 21 families were sorted and identified in this study.

Insect vectors were captured in seven different plant families: Apiaceae, Asteraceae, Boraginaceae, Convolvulaceae, Dipsacaceae, Malvaceae and Scrophulariaceae. The most represented families in terms of plant species diversity were Asteraceae and Apiaceae, respectively presenting about 33% and 21% of collected plant species. *Philaenus tesselatus* was the most captured vector species in Asteraceae, Apiaceae and in Oleaceae. The highest values of species richness in *X. fastidiosa* vectors were observed on Oleaceae (four species), Apiaceae (three species) and Convovulaceae (three species) (**Table 3.4**).

Xylella fastidiosa vector species were present in 15 different individual plant genera. The individual plant genus with the highest vector species diversity was *Convolvulus*, with *L. coleoptrata, N. campestris* and *P. tesselatus* captured (**Table 3.5**).

Insect vectors of *X. fastidiosa* were present in 16 different individual plant species. Among the identified plant species, five are in the European Commission list of plants found to be susceptible to *X. fastidiosa* in the EU: *Conium maculatum* L. (Apiaceae), *Daucus carota* L. (Apiaceae), *Heliotropium europaeum* L. (Boraginaceae), *Cistus salvifolius* L. (Cistaceae) and *Convolvulus arvensis* L. (Convolvulaceae) (EC, 2019). Some of the collected vector species were found in these susceptible plant species, except for *H. europaeum* and *C. salvifolius*. The only identified *P. spumarius* was found on *D. carota* (Apiaceae). *Cercopis intermedia* was not found in any of the 57 individual plant species, being captured exclusively in *Olea europea* L. (**Table 3.6**).

Concerning *O. europea* and mixed ground vegetation, olive trees were associated to the highest diversity of vector species, with four vector species, while in mixed ground vegetation only *P. tesselatus* was found (**Table 3.6**).

Table 3.4 –Total abundance (N), mean abundance and standard error of the mean (SE) of collected species of *Xylella fastidiosa* vectors per plant family.

Family	Family code	Number of genera	Number of species	Number of samples	*L. coleoptrata* N (Mean ± SE)	*N. campestris* N (Mean ± SE)	*Philaenus* sp. N (Mean ± SE)	*P. spumarius* N (Mean ± SE)	*P. tesselatus* N (Mean ± SE)	*C. intermedia* N (Mean ± SE)
Amaryllidaceae	AMARY	1	1	1	-	-	-	-	-	-
Apiaceae	APIAC	8	11	37	-	-	3 (0.08 ± 0.05)	1 (0.03 ± 0.03)	6 (0.16 ± 0.08)	-
Asparagaceae	ASPAR	1	1	1	-	-	-	-	-	-
Asteraceae	ASTER	15	19	57	-	-	4 (0.07 ± 0.03)	-	8 (0.14 ± 0.06)	-
Boraginaceae	BORAG	3	3	18	-	-	2 (0.11 ± 0.11)	-	2 (0.11 ± 0.08)	-
Brassicaceae	BRASS	2	2	5	-	-	-	-	-	-
Caryophyllaceae	CARYO	1	1	1	-	-	-	-	-	-
Cistaceae	CISTA	1	2	3	-	-	-	-	-	-
Convolvulaceae	CONVO	1	2	11	2 (0.18 ± 0.18)	1 (0.09 ± 0.09)	-	-	1 (0.09 ± 0.09)	-
Dipsacaceae	DIPSA	1	1	5	-	-	1 (0.20 ± 0.20)	-	1 (0.20 ± 0.20)	-
Fabaceae	FABAC	1	2	3	-	-	-	-	-	-
Gentiaceae	GENTI	1	1	2	-	-	-	-	-	-
Geraniaceae	GERAN	1	1	1	-	-	-	-	-	-
Hypericaceae	HYPER	1	1	2	-	-	-	-	-	-
Malvaceae	MALVA	1	2	16	-	-	1 (0.06 ± 0.06)	-	3 (0.19 ± 0.14)	-
Papaveraceae	PAPAV	1	2	6	-	-	-	-	-	-
Plantaginaceae	PLANT	1	1	1	-	-	-	-	-	-
Primulaceae	PRIMU	1	1	1	-	-	-	-	-	-
Ranunculaceae	RANUN	1	1	1	-	-	-	-	-	-
Scrophulariaceae	SCROP	1	1	5	2 (0.40 ± 0.40)	-	-	-	-	-
Zygophyllaceae	ZYGOP	1	1	1	-	-	-	-	-	-
Oleaceae	OLEAC	1	1	95	-	4 (0.04 ± 0.02)	2 (0.02 ± 0.01)	-	27 (0.28 ± 0.06)	1 (0.01 ± 0.01)
Mixed ground cover	ESP	-	-	21	-	-	-	-	9 (0.43 ± 0.25)	-
Total		-	-	294	4 (0.01 ± 0.01)	5 (0.02 ± 0.01)	13 (0.04 ± 0.01)	1 (0.00 ± 0.00)	57 (0.19 ± 0.03)	1 (0.00 ± 0.00)

Table 3.5 – Total abundance (N), mean abundance and standard error of the mean (SE) of collected species of *Xylella fastidiosa* vectors per plant genus.

Plant family	Plant genus	Genus code	Number of plant species	Number of samples	*L. coleoptrata* N (Mean ± SE)	*N. campestris* N (Mean ± SE)	*Philaenus* sp. N (Mean ± SE)	*P. spumarius* N (Mean ± SE)	*P. tesselatus* N (Mean ± SE)	*C. intermedia* N (Mean ± SE)
Amaryllidaceae	*Allium*	ALLIU	1	1	-	-	-	-	-	-
Apiaceae	*Ammi*	AMMI	1	1	-	-	-	-	-	-
	Cachrys	CACHR	1	4	-	-	-	-	-	-
	Conium	CONIU	1	1	-	-	-	-	1 (1.00 ± 0.00)	-
	Daucus	DAUCU	3	21	-	-	2 (0.10 ± 0.07)	1 (0.05 ± 0.05)	-	-
	Elaeoselinum	ELAEO	1	2	-	-	-	-	2 (1.00 ± 1.00)	-
	Foeniculum	FOENI	1	3	-	-	1 (0.33 ± 0.33)	-	-	-
	Ridolfia	RIDOL	1	2	-	-	-	-	2 (1.00 ± 1.00)	-
	Torilis	TORIL	2	3	-	-	-	-	1 (0.33 ± 0.33)	-
Asparagaceae	*Ornithogalum*	ORNIT	1	1	-	-	-	-	-	-
Asteraceae	*Anacyclus*	ANACY	1	8	-	-	-	-	-	-
	Andryala	ANDRY	2	14	-	-	2 (0.14 ± 0.10)	-	1 (0.07 ± 0.07)	-
	Calendula	CALEN	1	1	-	-	-	-	-	-
	Carduus	CARDU	1	2	-	-	-	-	-	-
	Chamaemelum	CHAMA	1	10	-	-	-	-	4 (0.40 ± 0.27)	-
	Chrysanthemum	CHRYS	2	5	-	-	-	-	-	-
	Cichorium	CICHO	1	3	-	-	-	-	-	-
	Conyza	CONYZ	1	1	-	-	-	-	-	-
	Crepis	CREPI	3	5	-	-	-	-	1 (0.20 ± 0.20)	-
	Galactites	GALAC	1	3	-	-	2 (0.67 ± 0.33)	-	2 (0.67 ± 0.67)	-
	Mantisalca	MANTI	1	1	-	-	-	-	-	-
	Pulicaria	PULIC	1	1	-	-	-	-	-	-
	Scolymus	SCOLY	1	1	-	-	-	-	-	-
	Tolpis	TOLPI	1	1	-	-	-	-	-	-

Table 3.5 (cont.) – Total abundance (N), mean abundance and standard error of the mean (SE) of collected species of *Xylella fastidiosa* vectors per plant genus.

Plant family	Plant genus	Genus code	Number of plant species	Number of samples	*L. coleoptrata* N (Mean ± SE)	*N. campestris* N (Mean ± SE)	*Philaenus* sp. N (Mean ± SE)	*P. spumarius* N (Mean ± SE)	*P. tesselatus* N (Mean ± SE)	*C. intermedia* N (Mean ± SE)
Asteraceae (cont.)	*Urospermum*	UROSP	1	1	-	-	-	-	-	-
Boraginaceae	*Anchusa*	ANCHU	1	1	-	-	-	-	-	-
	Echium	ECHIU	1	15	-	-	2 (0.13 ± 0.13)	-	2 (0.13 ± 0.09)	-
	Heliotropium	HELIO	1	2	-	-	-	-	-	-
Brassicaceae	*Hirschfeldia*	HIRSC	1	4	-	-	-	-	-	-
	Raphanus	RAPHA	1	1	-	-	-	-	-	-
Caryophyllaceae	*Spergularia*	SPERG	1	1	-	-	-	-	-	-
Cistaceae	*Cistus*	CISTU	2	3	-	-	-	-	-	-
Convolvulaceae	*Convolvulus*	CONVO	2	11	2 (0.18 ± 0.18)	1 (0.09 ± 0.09)	-	-	1 (0.09 ± 0.09)	-
Dipsacaceae	*Scabiosa*	SCABI	1	5	-	-	1 (0.20 ± 0.20)	-	1 (0.20 ± 0.20)	-
Fabaceae	*Ononis*	ONONI	2	3	-	-	-	-	-	-
Gentiaceae	*Centaurium*	CENTA	1	2	-	-	-	-	-	-
Geraniaceae	*Erodium*	ERODI	1	1	-	-	-	-	-	-
Hypericaceae	*Hypericum*	HYPER	1	2	-	-	-	-	-	-
Malvaceae	*Lavatera*	LAVAT	2	16	-	-	1 (0.06 ± 0.06)	-	3 (0.19 ± 0.14)	-
Papaveraceae	*Papaver*	PAPAV	2	6	-	-	-	-	-	-
Plantaginaceae	*Linaria*	LINAR	1	1	-	-	-	-	-	-
Primulaceae	*Anagallis*	ANAGA	1	1	-	-	-	-	-	-
Ranunculaceae	*Nigella*	NIGEL	1	1	-	-	-	-	-	-
Scrophulariaceae	*Verbascum*	VERBA	1	5	2 (0.40 ± 0.40)	-	-	-	-	-
Zygophyllaceae	*Tribulus*	TRIBU	1	1	-	-	-	-	-	-
Oleaceae	*Olea*	OLEA	1	95	-	4 (0.04 ± 0.02)	2 (0.02 ± 0.01)	-	27 (0.28 ± 0.06)	1 (0.01 ± 0.01)
Mixed ground cover		MIX	-	21	-	-	-	-	9 (0.43 ± 0.25)	-
Total				294	4 (0.01 ± 0.01)	5 (0.02 ± 0.01)	13 (0.04 ± 0.01)	1 (0.00 ± 0.00)	57 (0.19 ± 0.03)	1 (0.00 ± 0.00)

Table 3.6 – Total abundance (N), mean abundance and standard error of the mean (SE) of collected species of *Xylella fastidiosa* vectors per plant species; plants susceptibility to the phytopathogen in the European Union according to EC (2019) are indicated with an asterisk.

Plant family	Plant species	Species code	Number of samples	*L. coleoptrata* N (Mean ± SE)	*N. campestris* N (Mean ± SE)	*Philaenus* sp. N (Mean ± SE)	*P. spumarius* N (Mean ± SE)	*P. tesselatus* N (Mean ± SE)	*C. intermedia* N (Mean ± SE)
Amaryllidaceae	*Allium ampeloprasum* L.	ALAM	1	-	-	-	-	-	-
Apiaceae	*Ammi majus* L.	AMMA	1	-	-	-	-	-	-
	Cachrys sicula L.	CASI	4	-	-	-	-	-	-
	**Conium maculatum* L.	COMA	1	-	-	-	-	1 (1.00 ± 0.00)	-
	**Daucus carota* L.	DACA	16	-	-	2 (0.13 ± 0.09)	1 (0.06 ± 0.06)	-	-
	Daucus crinitus Desf.	DACR	1	-	-	-	-	-	-
	Daucus muricatus (L.) L.	DAMU	4	-	-	-	-	-	-
	Elaeoselinum foetidum (L.) Boiss.	ELFO	2	-	-	-	-	2 (1.00 ± 1.00)	-
	Foeniculum vulgare Mill.	FOVU	3	-	-	1 (0.33 ± 0.33)	-	-	-
	Ridolfia segetum (L.) Moris	RISE	2	-	-	-	-	2 (1.00 ± 1.00)	-
	Torilis arvensis (Huds.) Link	TOAR	2	-	-	-	-	-	-
	Torilis sp.	TOSP	1	-	-	-	-	1 (1.00 ± 0.00)	-
Asparagaceae	*Ornithogalum narbonense* L.	ORNA	1	-	-	-	-	-	-
Asteraceae	*Anacyclus radiatus* Loisel.	ANRA	8	-	-	-	-	-	-
	Andryala integrifolia L.	ANIN	10	-	-	2 (0.20 ± 0.13)	-	1 (0.10 ± 0.10)	-
	Andryala laxiflora DC.	ANLA	4	-	-	-	-	-	-
	Calendula arvensis L.	CAAR	1	-	-	-	-	-	-
	Carduus tenuiflorus Curtis	CATE	2	-	-	-	-	-	-
	Chamaemelum mixtum (L.) All.	CHMI	10	-	-	-	-	4 (0.40 ± 0.27)	-
	Chrysanthemum coronarium L.	CHCO	4	-	-	-	-	-	-
	Chrysanthemum segetum L.	CHSE	1	-	-	-	-	-	-
	Cichorium intybus L.	CIIN	3	-	-	-	-	-	-
	Conyza bonariensis (L.) Cronquist	COBO	1	-	-	-	-	-	-
	Crepis capillaris (L.) Wallr.	CRCA	3	-	-	-	-	1 (0.33 ± 0.33)	-
	Crepis sp.	CRSP	1	-	-	-	-	-	-
	Crepis vesicaria L.	CRVE	1	-	-	-	-	-	-
	Galactites tomentosus Moench	GATO	3	-	-	2 (0.67 ± 0.33)	-	2 (0.67 ± 0.67)	-
	Mantisalca salmantica (L.) Briq. & Cavill.	MASA	1	-	-	-	-	-	-
	Pulicaria paludosa Link	PUPA	1	-	-	-	-	-	-
	Scolymus hispanicus L.	SCHI	1	-	-	-	-	-	-

Table 3.6 (cont.) – Total abundance (N), mean abundance and standard error of the mean (SE) of collected species of *Xylella fastidiosa* vectors per plant species; plants susceptibility to the phytopathogen in the European Union according to EC (2019) are indicated with an asterisk.

Plant family	Plant species	Species code	Number of samples	*L. coleoptrata* N (Mean ± SE)	*N. campestris* N (Mean ± SE)	*Philaenus* sp. N (Mean ± SE)	*P. spumarius* N (Mean ± SE)	*P. tesselatus* N (Mean ± SE)	*C. intermedia* N (Mean ± SE)
Asteraceae (cont.)	*Tolpis barbata* (L.) Gaertn.	TOBA	1	-	-	-	-	-	-
	Urospermum picroides (L.) F.W.Schmidt	URPI	1	-	-	-	-	-	-
Boraginaceae	*Anchusa azurea* Mill.	ANAZ	1	-	-	-	-	-	-
	Echium plantagineum L.	ECPL	15	-	-	2 (0.13 ± 0.13)	-	2 (0.13 ± 0.09)	-
	**Heliotropium europaeum* L.	HEEU	2	-	-	-	-	-	-
Brassicaceae	*Hirschfeldia incana* (L.) Lagr.-Foss.	HIIN	4	-	-	-	-	-	-
	Raphanus raphanistrum L.	RARA	1	-	-	-	-	-	-
Caryophyllaceae	*Spergularia purpurea* (Pers.) G.Don	SPPU	1	-	-	-	-	-	-
Cistaceae	*Cistus crispus* L.	CICR	1	-	-	-	-	-	-
	**Cistus salvifolius* L.	CISA	2	-	-	-	-	-	-
Convolvulaceae	*Convolvulus althaeoides* L.	COAL	2	-	-	-	-	-	-
	**Convolvulus arvensis* L.	COAR	9	2 (0.22 ± 0.22)	1 (0.11 ± 0.11)	-	-	1 (0.11 ± 0.11)	-
Dipsacaceae	*Scabiosa atropurpurea* L.	SCAT	5	-	-	1 (0.20 ± 0.20)	-	1 (0.20 ± 0.20)	-
Fabaceae	*Ononis pubescens* L.	ONPU	2	-	-	-	-	-	-
	Ononis viscosa L.	ONVI	1	-	-	-	-	-	-
Gentiaceae	*Centaurium pulchellum* (Sw.) Druce	CEPU	2	-	-	-	-	-	-
Geraniaceae	*Erodium moschatum* (L.) L'Hér.	ERMO	1	-	-	-	-	-	-
Hypericaceae	*Hypericum perforatum* L.	HYPE	2	-	-	-	-	-	-
Malvaceae	*Lavatera cretica* L.	LACR	13	-	-	1 (0.08 ± 0.08)	-	2 (0.15 ± 0.15)	-
	Lavatera trimestris L.	LATR	3	-	-	-	-	1 (0.33 ± 0.33)	-
Papaveraceae	*Papaver dubium* L.	PADU	1	-	-	-	-	-	-
	Papaver rhoeas L.	PARH	5	-	-	-	-	-	-
Plantaginaceae	*Linaria spartea* (L.) Chaz.	LISP	1	-	-	-	-	-	-
Primulaceae	*Anagallis arvensis* L.	ANAR	1	-	-	-	-	-	-
Ranunculaceae	*Nigella damascena* L.	NIDA	1	-	-	-	-	-	-
Scrophulariaceae	*Verbascum sinuatum* L.	VESI	5	2 (0.40 ± 0.40)	-	-	-	-	-
Zygophyllaceae	*Tribulus terrestris* L.	TRTE	1	-	-	-	-	-	-
Oleaceae	**Olea europaea* L.	OLEU	95	-	4 (0.04 ± 0.02)	2 (0.02 ± 0.01)	-	27 (0.28 ± 0.06)	1 (0.01 ± 0.01)
Mixed ground cover		MIX	21	-	-	-	-	9 (0.43 ± 0.25)	-
Total			294	4 (0.01 ± 0.01)	5 (0.02 ± 0.01)	13 (0.04 ± 0.01)	1 (0.00 ± 0.00)	57 (0.19 ± 0.03)	1 (0.00 ± 0.00)

3.7. Effect of environmental factors on *Xylella fastidiosa* vectors

The summary of abundance of collected *X. fastidiosa* vectors by the 22 analysed environmental factors can be found in **Annex F: Table F.1.** Kruskal-Wallis tests did not show any significant differences of vector's abundance among classes of all independent variables (**Annex F: Table F.2**), except for the dependent/independent variables combinations shown in **Table 3.7**. ANOVA test results on the ranked abundances for these dependent/independent variable combinations (**Annex F: Table F.3**), posteriorly discriminated by the Fisher's LSD test at the 0.05 level of significance (**Annex F: Tables F.4**) are also available.

Table 3.7 – Results of Kruskal-Wallis tests with statistical significance (p-value ≤ 0.05) comparing the variation of abundance of different species of *Xylella fastidiosa* vectors among classes from multiple environmental variables. N = number of samples; df = degrees of freedom; χ^2 = Kruskal-Wallis test statistic.

Dependent variable	Independent variable	N	df	χ^2	p-value
Lepyronia coleoptrata	Geographic unit	150	17	45.1782	***
	Plant family	170	12	22.8626	*
Neophilaenus campestris	Area of vineyards in 250 m radius	150	2	6.2775	*
	Area of cork oak in 250 m radius	150	2	6.9707	*
Philaenus tesselatus	Total precipitation	150	3	11.7718	**
	Area of olive groves in 250 m radius	150	5	11.3933	*
Philaenus sp.	Geographic unit	150	17	37.7143	**
	Host plant	150	1	5.0067	*
	Mean temperature	149	3	16.7240	***
	Area of olive groves in 250 m radius	150	5	14.8527	*

Note: *p<0.05, **p<0.005 e ***p<0.000

In the case of the *P. spumarius*, Fisher's LSD test was not performed, as only one individual was found, the same with the combination *Philaenus* sp./Host, as the independent variable consists of only two different classes.

Lepyronia coleoptrata showed significant differences in abundance between different GU's, being found only in GU3 and GU21, the first located in the northeast part and the second in the southeast part of Alentejo (**Annex B: Figure B. 1**). The abundance of *L. coleoptrata* was about four times higher in GU3 (**Figure 3.9A**). *Lepyronia coleoptrata* was only captured in the plant families Convolvulaceae and Scrophulariaceae, being more abundant in the last family mentioned (**Figure 3.9B**).

Neophilaenus campestris showed significant differences in abundance between varying proportions of area occupied by vineyards and by cork oak in a 250 m radius. The results showed that in, both cases, the existence of vineyards and cork oak in the vicinity of the sampling points seems to be associated with higher abundance of *N. campestris* (**Figure 3.10**).

Philaenus tesselatus showed significant differences in abundance per total precipitation and per proportion of area of olive groves in 250 m radius. *Philaenus tesselatus* showed higher abundance when the precipitation was the lowest (5 mm) and highest (50 mm), but with no significant differences between these precipitation values (**Figure 3.11A**). The existence of olive groves in a 250 m radius seems to not, in the case of *P. tesselatus*, have an apparent visible pattern (**Figure 3.11B**).

Philaenus sp. showed significant differences in abundance between different GU´s located, in general, in the north part of the study area (**Figure B. 1**). The highest abundance was found in GU4, GU6 and GU7 (with no significant differences between them) and the lowest in the GU0, GU9 and GU15, also with no significant differences between each other, showing no apparent pattern (**Figure 3.12A**). Regarding the host plant, the abundance of *Philaenus* sp. on ground vegetation seems to be almost 10 times higher than on olives (**Figure 3.12B**). Mean temperature seems to affect the abundance of

Philaenus sp., which shows higher vector abundance around 24 ºC than in both lower and higher temperatures (**Figure 3.12C)**. Lastly, the abundance of *Philaenus* sp. seems to vary with the percentage of area of olive groves in the vicinity of sampling points, showing higher abundance when the proportion of olive groves in the neighbourhood is between 50 and 75% (**Figure 3.12D**).

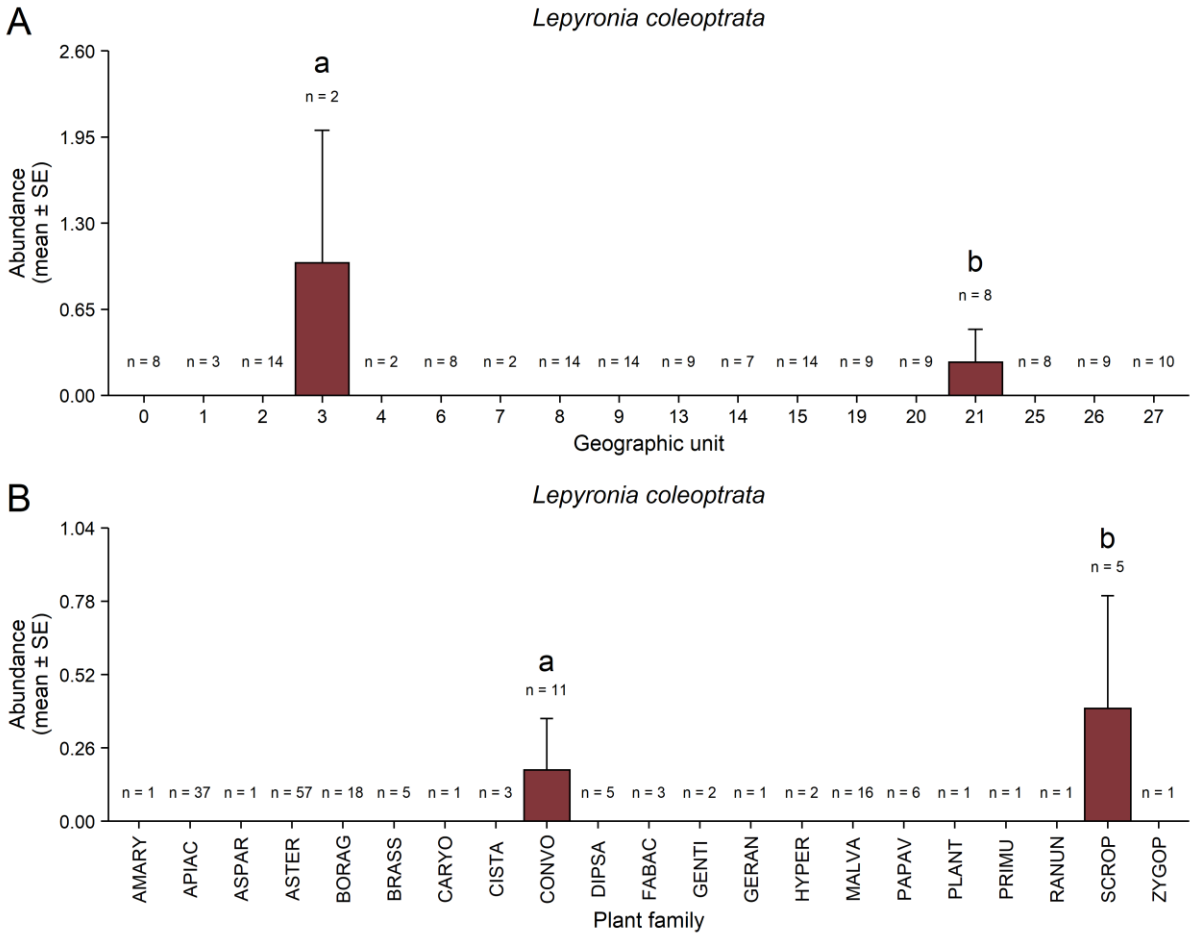

Figure 3.9 – Mean abundance of *Lepyronia coleoptrata* by different factors. **A** – Geographic unit. **B** – Plant family. n = number of samples; SE = standard error of the mean; AMARY = Amaryllidaceae; APIAC = Apiaceae; ASPAR = Asparagaceae; ASTER = Asteraceae; BORAG = Boraginaceae; BRASS = Brassicaceae; CARYO = Caryophyllaceae; CISTA = Cistaceae; CONVO = Convolvulaceae; DIPSA = Dipsacaceae; FABAC = Fabaceae; GENTI = Gentiaceae; HYPER = Hypericaceae; MALVA = Malvaceae; PAPAV = Papaveraceae; PLANT = Plantaginaceae; PRIMU = Primulaceae; RANUN = Ranunculaceae; SCROP = Scrophulariaceae; ZYGOP = Zygophillaceae. Bars with the same letter are not significantly different by the Fisher's LSD test at the 0.05 level of significance. Fisher's LSD tests were applied only when Kruskal-Wallis test showed significant differences.

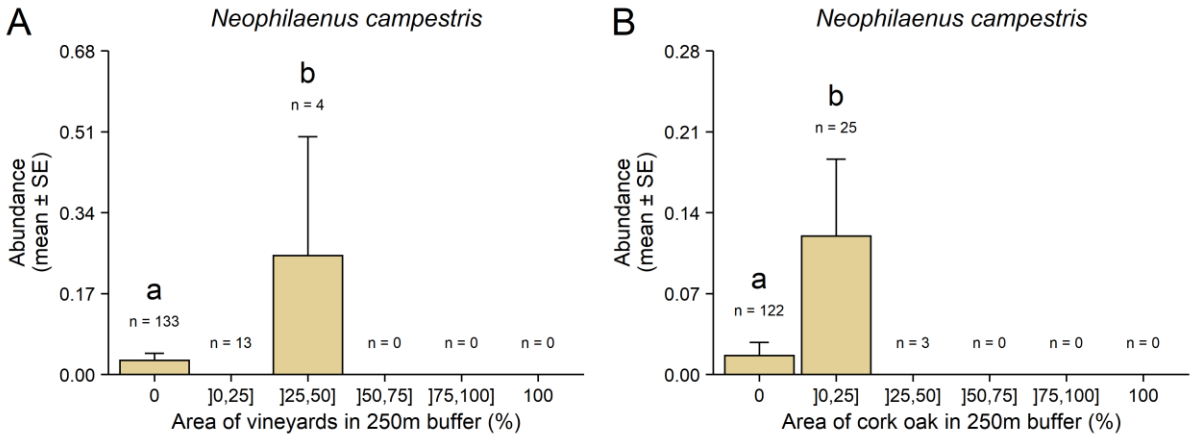

Figure 3.10 – Mean abundance of *Neophilaenus campestris* by different factors. **A** – Percentage of area of vineyards in 250 m radius. **B** – Percentage and area of cork oak in 250 m radius. n = number of samples; SE = standard error of the mean. Bars with the same letter are not significantly different by the Fisher's LSD test at the 0.05 level of significance. Fisher's LSD tests were applied only when Kruskal-Wallis test showed significant differences.

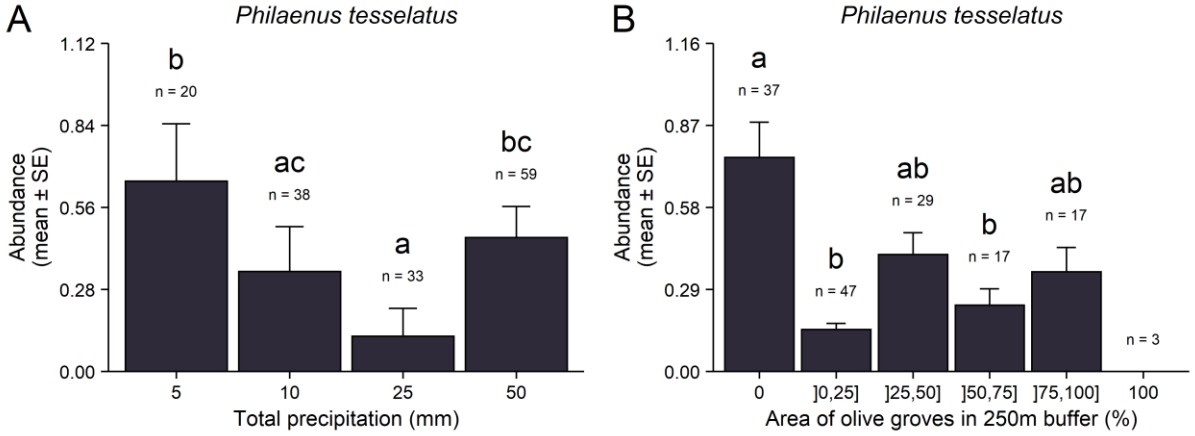

Figure 3.11 – Mean abundance of *Philaenus tesselatus* by different factors. **A** – Total precipitation. **B** – Percentage of area of olive groves in 250 m radius. n – number of samples; SE = standard error of the mean. Bars with the same letter are not significantly different by the Fisher's LSD test at the 0.05 level of significance. Fisher's LSD tests were applied only when Kruskal-Wallis test showed significant differences.

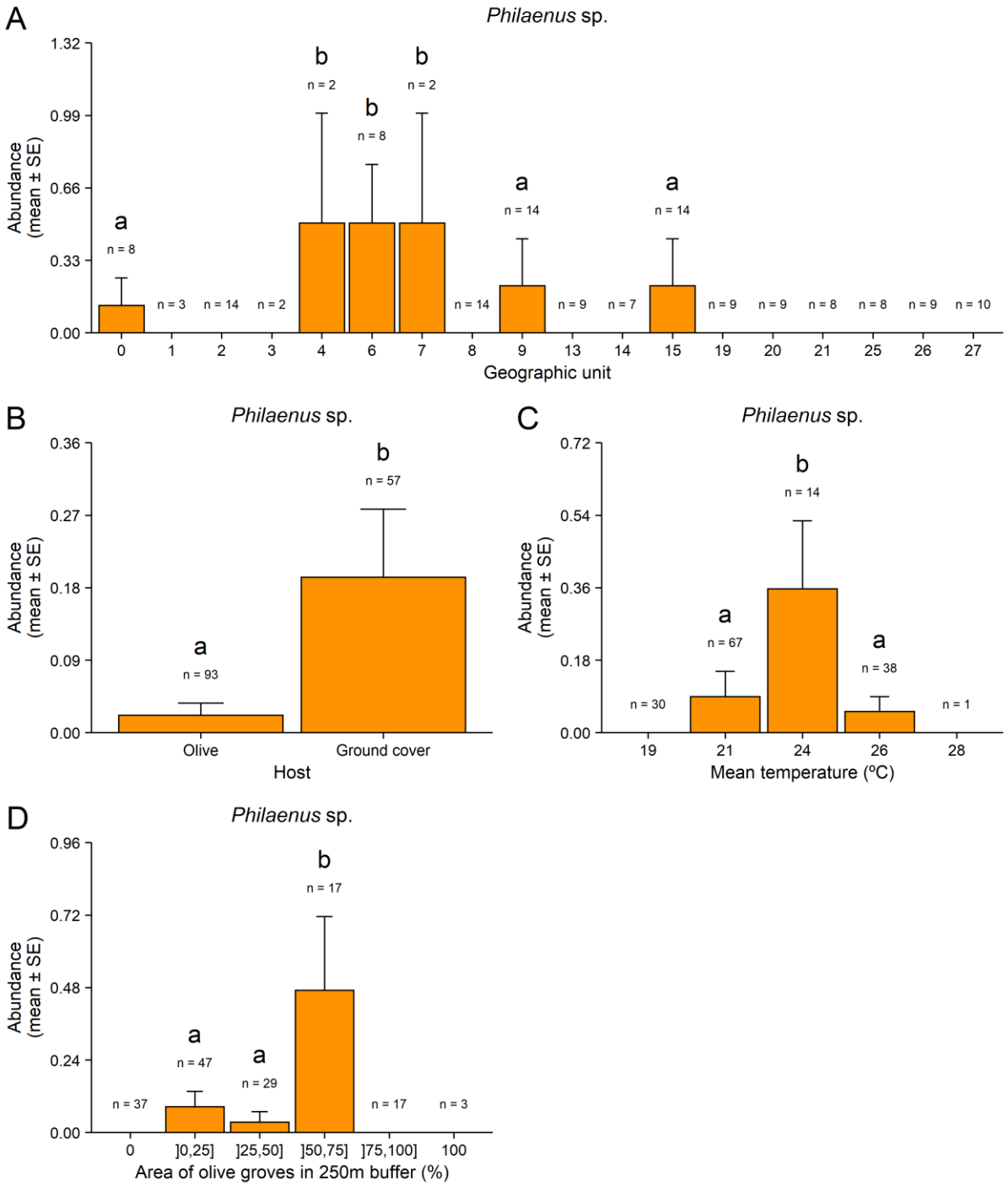

Figure 3.12 - Mean abundance of *Philaenus* sp. by different factors. **A** – Geographic unit. **B** – Plant host. **C** – Mean temperature. **D** – Percentage of area of olive groves in 250 m radius. n – number of samples; SE = standard error of the mean. Bars with the same letter are not significantly different by the Fisher's LSD test at the 0.05 level of significance. Fisher's LSD tests were applied only when Kruskal-Wallis test showed significant differences.

4. Discussion

4.1. Auchenorrhyncha and *Xylella fastidiosa* vectors

4.1.1. Xylella fastidiosa vectors

In this study, five vectors/potential vectors were found: *P. spumarius*, *P. tesselatus*, *C. intermedia*, *L. coleoptrata* and *N. campestris*. According to the results, *P. tesselatus* was the most common species of spittlebugs, with a wide distribution in the Alentejo Region. The *Philaenus* sp. individuals, found both in this study and in the previous study conducted in autumn of 2016 by Neto (2017), were all female, making further identification, based on morphology, not possible. Neto (2017) speculated that the individuals might belong to *P. tesselatus* and the results, in this study, confirm that it is likely possible that the female individuals found in both studies are *P. tesselatus*. Only one male of *P. spumarius* was found in the northwest of the study area. The isolated individual of *P. spumarius* found cannot be considered unusual, since it is known that *P. spumarius* occurs in Portuguese mainland but tend to concentrate more in the north of Lisbon while *P. tesselatus* is more abundant to the south of Lisbon (Drosopoulos & Quartau, 2002). In this study no nymphs of *Philaenus* sp. were found. Although this spittlebug is univoltine (Brakefield,1990), temperature can influence the development rate of different life stages (Yurstsever, 2000). For example, in colder regions, development to the adult stage takes longer, egg hatching begins in April and adults appear in June (Yurtsever, 2000). In Mediterranean climate, like in Italy, the nymphal stages are possible to detected, starting from the second week of March, while the first adults started to appear from late April to early May (Bodino et al., 2019b). In Portugal, Rodrigues (2010) reported observation of the first instar nymphs as early as February, with the first adults detected in April. Given that the sampling period in this study was from 3rd of May to 8th of June, it is plausible that no nymphs were observed, as they were already adults.

Philaenus tesselatus status as a species is still in discussion, being treated as a subspecies of *P. spumarius* by some authors (Nska-Nadachowska et al., 2011) and as a species by others (Drosopoulos & Quartau, 2002; Seabra et al., 2019). According to the morphological data, *P. spumarius* is consistently smaller than *P. tesselatus*, with no intermediate forms (Drosopoulos & Quartau, 2002), which is consistent with the findings in this study **Figure 3.5**: **A, B** , as well as a clear difference in aedeagus morphology, especially in the upper and lower appendages, with *P. tesselatus* presenting always larger measurements than *P. spumarius* **Figure 3.6: A, B** (Drosopoulos & Quartau, 2002; Seabra et al., 2019). However, genomic assessment shows conflicting results, with no difference between *P. spumarius* and *P. tesselatus* at mitochondrial DNA, presenting the same haplotypes (Seabra at al., 2019) - "combination of alleles at different markers along the same chromosome that are inherited as a unit" (Crawford & Nickerson, 2005), but also showing a differentiation at genome-wide makers between *P. spumarius* and *P. tesselatus* (Nska-Nadachowska et al., 2011; Seabra et al., 2019). Being able to correctly identify the species is very important as it is directly related to the establishment of efficient control practices of the insect vectors and disease management.

Philaenus spp. adults present a balanced polymorphism (Yurtsever, 2001) showing striking dorsal colour patterns, with *P. spumarius* having at least sixteen naturally occurring phenotypes (Yurtsever, 2000). Thirteen phenotypes have been reported in mainland Portugal (Quartau & Borges, 1997), of which six were found in this study. The most frequent phenotypes found in Alentejo Region were non-melanic, more specifically, *populi* and *typicus*, coinciding with the result of Neto (2017), which also found these two phenotypes to be more frequent. In Portugal, the tendency between male and female is, for the first, to present majorly non-melanic phenotypes while the females tend to present more frequently melanic dorsal colour patterns (Quartau & Borges, 1997). In other populations, like in Britain

and Turkey, no obvious differences between the sexes regarding colour pattern frequencies have been noted (Stewart & Lees, 1988; Yurtsever, 2000) In the present study no tendency in colour pattern between the sexes was observed probably because the size of the sample was too small. The occurrence of the phenotypes and their frequency may vary among natural populations, the variation being linked to habitat composition (Quartau & Borges, 1997), climate conditions (Halkka, 1964; Halkka et al., 1975; 1980), atmospheric pollution (Lees & Dent, 1983) or gender (Quartau & Borges, 1997; Yurtsever, 2000).

As mentioned before, *P. tesselatus* was the most captured vector species in Asteraceae, Apiaceae and in Oleaceae. The only identified *P. spumarius* was captured in Apiaceae (*D. carota*) as well, showing a preference for these plant families in Alentejo olive groves. Similar tendency occurred in Italian olive groves, in the Apulian and Liguria regions, where a preference of *P. spumarius* for Apiaceae, as well for Asteraceae and Fabaceae (Bodino et al., 2020; Dongiovanni et al., 2019) was observed. The highest vector species diversity was found in the plant genus *Convolvulus*, although not the one with the highest abundance of vectors, but still, as a plant found to be susceptible to *X. fastidiosa* in the EU (EC, 2019), its presence near the olive trees should be monitored.

In the study conducted in autumn by Neto (2017), potential vectors were more frequently present on weeds, however in this work only *Philaenus* sp. showed higher abundance on ground vegetation than on olive trees. No other potential vector presented significant statistical results regarding host preference. In the study area, during sample collection, a significant amount of green herbaceous vegetation surrounding the olive grove could be observed, since months prior to the sampling period were rainy. Only April showed low total precipitation, spiking again in May, with March being the wettest month that year (**Figure 3.1**). This could mean that, the green ground cover was potentially, at least, as attractive to the vectors as the olive trees. Interestingly, different abundance of spittlebugs was also found in different olive orchards, in different regions in Italy and Greece. In Italy, the olive orchards in drier climate presented a lower number of spittlebugs as well as the rainfed olive groves in Greece, showing a preference of the spittlebugs for plants with lower water stress (Bodino et al., 2020; Tsagkarakis et al., 2018). These results suggest that a difference in crop management might contribute to the presence of vectors and consequent spread of the phytopathogen.

The higher number of spittlebugs present in herbaceous vegetation during autumn in Alentejo Region could be due to the oviposition behaviour of spittlebugs, as the eggs are laid close to the ground (Weaver & King, 1954). This could be considered a pivotal moment in the biological life cycle of this spittlebug as the adult individuals seem to lessen their migratory activity (Weaver & King, 1954) and an application of control measures can be more effective at this time than during the rest of the year (Bodino et al., 2020). Also, special attention should be payed to the herbaceous vegetation, in the vicinity of the olive orchards, specially to the plant families which the vector species showed preference, as they can host a considerate number of spittlebugs and be an attractive place for oviposition. The elimination or limitation of these plant species can limit the number of nymph present close to the olive orchards. Dongiovanni et al. (2019) data also suggested that if nymph populations are left unmonitored, there is a higher chance of an elevated number of adult emerge and move to the olive trees, where they can acquire and transmit *X. fastidiosa* (Cornara et al., 2017), recommending that soil tiling, correctly timed, applied at the peak of nymphal population can limit the emergence of adults.

Precipitation and temperature are dominant abiotic factors that affect the distribution and population dynamics of both insects and vegetation, modulating insect-plant interactions in the case of herbivorous insects (Halkka et al., 2006) and have been linked to impact the *X. fastidiosa* establishment and spread (Bosso et al., 2016a; 2016b). For example, egg hatching of the meadow spittlebug occurs between 10 and 21 °C (Weaver and King, 1954) and the lower and upper threshold for nymphal development are

2.8 and 26.7 °C, respectively (Chmiel & Wilson, 1979). Halkka et al. (2006) showed that nymph mortality caused by desiccation was linked to climatic variables, influencing the abundance of *P. spumarius*. Neto (2017) reported low numbers of *Philaenus* sp. in the collected samples (only five specimens), hypothesizing that the extreme climatic conditions taking place during summer (with higher than average temperature and precipitation values lower than average, since 1931) (IPMA, 2016) impacted *Philaenus* sp. populations. The results displayed in this study support such hypothesis, as *P. tesselatus* presented significant differences in abundance per total precipitation in olive groves in the Alentejo Region and *Philaenus* sp. showed significant differences regarding mean temperature, with higher abundance at 24 °C, which is consistent with the optimal development temperature for insects in temperate regions (Rodrigues, 2004). The survival of *Philaenus* spp. in more extreme climate conditions related to lower precipitation and higher temperatures could be severely limited. Although several older studies on the influence of temperature on spittlebug development are available, new studies are needed to fill the gap (Cornara et al., 2018).

When it comes to the spread of the bacterium in adverse climates, Bosso et al. (2016a; 2016b) showed that precipitation of driest quarter, mean temperature of coldest and warmest quarter influence the potential distribution of the bacterium in Italy and in the Mediterranean region. Godefroid et al. (2019) also evaluated the potential climate suitability of European continent for the *X. fastidiosa* subsp. *fastidiosa*, *X. fastidiosa* subsp. *pauca* and *X. fastidiosa* subsp. *multiplex* by using species distribution modelling, determining that the currently reported geographical range of the bacterium in Europe is small compared to the large extent of climatically suitable zones and that the distribution of the three subspecies appeared to be limited by minimum winter temperatures, with *X. fastidiosa* subsp. *pauca* being more sensible than the others. This is consistent with what was previously described by Hopkins and Purcell (2002) in Californian grapevines, where the cold winter is unfavourable for bacterial colonization, limiting *X. fastidiosa* to small branches in which the bacterium is more vulnerable to cold temperatures and can be removed by winter pruning. Specifically, Lieth et al. (2011) found that temperatures below < 6 °C kill *X. fastidiosa* with increasing efficacy. With climate change, the minimum winter temperatures are likely to increase, altering the distribution of *X. fastidiosa* (Daugherty et al., 2017; Freil & Purcell, 2001). On the other hand, the impact of high temperatures on *X. fastidiosa* is still poorly known, however Freil & Purcell (2001) revealed that this phytopathogen decreases when exposed to temperatures above 37 ºC, both *in vitro* and in potted grapevines and determined that the minimum threshold temperatures for growth of *X. fastidiosa* in plants to be between 17 and 25 °C.

The climate conditions reported in Portugal for 2017 (**Figure 3.1**), as well as today (IPMA, 2020a, 2020b), are favourable for *Philaenus* spp. and *X. fastidiosa*, and can potentially have severe impacts in olive orchards, if the bacterium reaches the Alentejo Region. However, future climate change projections for the Alentejo Region hint at a general increase in temperatures and a decrease in precipitation, as well as a higher occurrence of extreme climatical events, such as heatwaves, droughts, storms, among others (Fraga et al., 2018; Fraga & Santos, 2018; Giorgi & Lionello, 2008; Santos et al., 2017), which will affect the distribution and dynamics of vector populations, host plants growth, the efficiency of pathogen transmission and vector/host plant dynamics.

The limitations of the data used in this study must be recognised, as the precipitation and temperature used for the statistical analysis was from the Mensal Climatological Bulletins, the precipitation/temperature values were grouped in classes, which resulted in four classes with one precipitation/temperature value. Yet by doing so, there are no variations in the classes and, an artificiality of the data occurs. To have an authenticity to the climatological variables in the Alentejo Region the precipitation/temperature should be recorded every day.

Interestingly, the abundance of *P. tesselatus* showed no apparent visible pattern when analysing the existence of the olive groves in a 250 m radius, while *Philaenus* sp. showed higher abundance when the proportion of the olive groves in the vicinity was 50% or higher. Also, *Philaenus* sp. showed significant differences in abundance between different GU´s, but with no apparent pattern between them and while there were no statistical differences in the preference of the plant host in *P. tesselatus*, *Philaenus* sp. showed a preference for ground vegetation. These results are inconsistent and probably so because the *Philaenus* sp. is likely to be *P. tesselatus* as well and by analysing them separately we are slightly altering the bigger picture and attributing or taking away significance to/of the variables.

Neophilaenus campestris, a spittlebug widespread in Europe and in many other Mediterranean countries (Drosopoulos & Remane, 2000), with a life cycle very similar to *P. spumarius* (Mazonni et al., 2005), was also found in this study, as well as in the autumn samples, although in low abundance in both studies (five specimens in this study and twenty in the autumn samples). *N. campestris* can be commonly found in grasslands (Poaceae) but can also be found on trees, seeking shelter during hot days, like for example on cypress (Mazzoni et al., 2005). Despite the low abundance, this spittlebug was present in olive trees (both in this study and in Neto 2017), as well as in *C. arvensis*.

Statistical analysis showed a correlation between the existence of vineyards and cork oak in the vicinity of the sampling points and the higher abundance of *N. campestris*. This tendency could be to the previously described behaviour of seeking shelter during the hot days, but further analysis is necessary since the number of captured individuals was too small. Cavalieri et al. (2019) demonstrated the transmission ability of *X. fastidiosa* by *N. campestris*, so, despite the observed low abundance of *N. campestris* in the Alentejo olive groves, this spittlebug represents a treat if *X. fastidiosa* reaches the region, not only to olive trees but to the surrounding cultures.

Only one female *C. intermedia* was found on olive trees in this study and no individuals of this species were found by Neto (2017), showing that *C. intermedia* does not have a noticeable presence in olive orchards in the Alentejo Region.

Lepyronia coleoptrata was found to be more abundant in the northeast part of the Alentejo Region, although a very limited number of individuals were captured in this study, and no *L. coleoptrata* individuals were captured in the autumn samples by Neto (2017). *Lepyronia coleoptrata* was only captured in the surrounding vegetation, a phenomenon observed as well in Greece by Antonatos et al. (2020) and in Spain, as both *L. coleoptrata* and *C. intermedia* were occasionally found on ground vegetation (Morente et al., 2018). In this study *L. coleoptrata* although also present in *C. arvensis* showed a preference for *Verbascum sinuatum* L. Since vector tendency and activity are key for the spread of the bacterium (Morente et al., 2018), the role of these species in the transmission of *X. fastidiosa* seems not significant or it should be limited.

Concluding, several factors play a role in *X. fastidiosa* disease spread including e.g., vector-host plant sensitivity, pathogen strain, host-pathogen interactions, microclimate conditions, landscape structure, and crop-management practices are also relevant (Godefroid et al., 2019; Redak et al. 2004; Sicard et al., 2018).

4.1.2. Other Auchenorrhyncha

The other species of Auchenorrhyncha that stood out the most in terms of abundance were *E. solani* and *Z. scuttelaris*, both species widely distributed in Europe. *Empoasca solani* is considered one of the main potato pests, occasionally ampelophagous, (Mazzoni et al., 2001), while *Z. scuttelaris* is a common maize pest, with no nefarious effect on the olive culture (Gabarra, 2017).

Several other species stood out as well, such as the subfamily Agallinae, known vectors of several diseases (Drobnjaković et al., 2010). *Anaceratagalia laevis* found in this study, is endemic to Europe (De Stradis et al., 2008) and is a vector of eggplant mottled dwarf virus (De Stradis et al., 2008), aster yellows and *Candidatus Phytoplasma solani* (stolbur phytoplasma) (Duduk et al., 2008).

Interestingly, in our survey, two individuals of *Arocephalus punctum* were found. This species can be commonly found in Denmark, Russia, Finland, Great Britain, Iceland, Italy, Norway, Sweden and Tunisia, but to the author's knowledge there are no previous records of this leafhopper in Portugal, with only *Arocephalus sagittarius* Ribaut reported in Portugal (Dmitriev, 2003-present).

Euscelidius variegatus was another Auchenorrhyncha captured that attracts attention, as it was also captured by Neto (2017) and in both studies on the herbaceous vegetation. *E. variegatus* is a known vector of several diseases such as aster yellows (Severin, 1947), *Chrysanthemum* yellows (D'Amelio et al., 2008). the corn stunt spiroplasma and the clover phyllody disease (Reis & Aguin-Pombo, 2003). In addition, in laboratory tests, it was also able to infect grapevine with *flavescência dorada* (Lherminier et al., 1990).

Euscelis alsius found in the ground vegetation, is a leafhopper, considered pest insect of an important seed crop, safflower (*Carthamus tinctorius* L.) in Iran (Saeidi & Adam, 2011). It also has been linked to citrus stubborn disease, testing positive for *Spiroplasma citri* in periwinkles in Morocco (Nhami et al., 1980).

The leafhopper *Neoliturus fenestratus* also found in this study, is a vector of safflower phyllody in Israel (Raccah & Klein, 1982) and causes lettuce phyllody and wild lettuce phyllody in Iran (Salehi et al. 2007). In vineyards in Israel (Orenstein et al. 2003), Czech Republic (Šafářová et al., 2018) and Spain (Batlle et al., 2000) specimens of *N. fenestratus* were reported to carry *Candidatus Phytoplasma solani* and aster yellows phytoplasma (wall-less bacteria that cause hundreds of plant diseases worldwide (Ivanauskas et al., 2011), making the leafhopper a potential threat to the vineyards in Europe due to its feeding habits (Orenstein et al. 2003) and due to its vector activity.

Five different individuals of the genus *Psammotettix* Haupt were identified in this study but were not possible to identify to the species. Despite that, a special attention should be paid to this result, since individuals of the genus *Psammotettix* have been found to be vectors of several diseases with economic impact (Greene, 1971). For example, *Psammotettix striatus* (L.), which has a worldwide distribution (including Portugal) (Dmitriev, 2003-present), is a vector to a phytoplasma that causes wheat blue dwarf in Western China, significantly limiting wheat production, making *P. striatus* one of the most significant economic pests of wheat in Western China (Zhao et al., 2010). Du et al. (2020) also confirmed the acquisition and transmission capabilities of wheat yellow striate virus by *Psammotettix alienus* (Dahlbom) and *Psammotettix provincialis* Ribaut has also been reported as a wheat dwarf virus vector (Parizipour et al., 2016).

Laodelphax striatella is a small brown planthopper with a worldwide distribution occurring from the Philippines to Scandinavia, mainly in the temperate zone (Kisimoto, 1989; Wang et al., 2017). It damages to plants comes not only from sap sucking but also by virus transmission (Kisimoto, 1989). It has been found to transmit various diseases of cereal, such as the rice stripe virus (Zang et al., 2007) and maize rough dwarf virus (Vidano, 1970).

The delphacid planthopper, *Metadelphax propinqua* was found in this study and in the autumn samples, mainly collected on weeds is both studies. *M. propinqua* vectors at least two plant diseases, such as maize rough dwarf disease and *Cynodon* chlorotic streak virus (Gonzon & Bartlett, 2007).

In our study, 88 % of the *Hyalesthes* individuals found were collected on *C. arvensis*. Studies has shown that not only this plant is susceptible to *X. fastidiosa* in the EU (EC, 2019), but also, it is a main host of *H. obsoletus* and *Candidatus Phytoplasma solani*, vector-borne phytoplasma which causes *bois noir*, an important grapevine yellows disease (Kosovac et al., 2019; Quaglino et al., 2013). *H. obsoletus* is also considered one of the main vectors of *bois noir* and is widespread in Central and Southern Europe, in the Near East and in the Mediterranean area (Lessio et al., 2007).

One individual of the genus *Macrosteles* Fieber was captured in our study. The leafhoppers of this genus are known for their vector activity. For example, *Macrosteles fascifrons* Stal (also known as *Macrosteles quadrilineatus* Forbes) is a vector for aster yellow vírus (Granados & Chapman, 1968) and a serious potato pest and other crops in the United States and Canada (Munyaneza et al., 2012). Also, *Macrosteles striifrons* Anufriev, *Macrosteles sexnotatus* (Fallén) are known vectors of phytopathogenic phytoplasmas (Ishii et al., 2013; Ivanauskas et al., 2011) and *Macrosteles laevis* Ribaut is one of the main vectors of *bois noir* (Bayram et al., 2014).

4.2. Natural enemies

One of the many ways of control of the vector population is by biological control, usually by parasitoid insects and/or arthropod predators. In this study, the most abundant or relevant taxa of parasitoids and predators found were Aranea, Coleoptera, Hemiptera and Hymenoptera. Although, none of the insects were identified past the taxon.

Most of parasitized specimens of Auchenorrhyncha were parasitized by Dryinidae, belonging to Hymenoptera, one of the most abundant taxa found in this study, with 13% of the collected specimens. Dryinidae are a common parasitoids and predators of Auchenorrhyncha (most commonly leafhoppers and planthoppers), characterized by the formation of a prominent sac (either black or dark), giving the larvae a semi-external position within the host (Waloff & Jervis, 1987).

In this study, the parasitized adult individuals belonged to the families Cicadellidae, Delphacidae and Deltocephalinae, while the nymphs belonged mostly to Cicadellidae, Issidae and Dictyopharidae. Coincidently, in the autumn samples, Neto (2017) also found individuals parasitized by Dryinidae, two delphacid adults and one delphacid nymph. Interestingly, Neto (2017), found one individual *N. campestris* parasitized by Dryinidae, while in our study none of the vectors or potential vectors were found parasitized. It is known that dryinids exert control over cicadellids, effectively helping maintain the populations under control (Giordano et al., 2002), but if the usual hosts of these parasitoids were lacking, could they adapt to parasitize spittlebugs?

Although found in lower abundancy, when compared to Hemiptera and Hymenoptera, significant number of spiders were accounted. The role of spiders as generalist predators in conservation biological control has long been studied (Maloney et al., 2003; Michalko et al., 2019; Nyffeler & Benz, 1987; Riechert & Lockley, 1984). Recently, Benhadi-Marín et al. (2020) designed a protocol to facilitate the targeting of spider species as potential natural enemies of *P. spumarius* in the olive crops in Northeastern Portugal. Further studies about the role of spiders as potential predators of *X. fastidiosa* vectors in Alentejo olive groves should be considered, as well as a potential implementation of this protocol.

Insects from the taxon Coleoptera has been shown to prey on *P. spumarius* (Harper & Whittaker, 1976). Also, *Zelus renardii* (Kolenati) (Hemiptera: Reduviidae), an American invasive species (Pinzari et al., 2018), through the years have been introduced in Europe, namely in Greece (Davranoglou, 2011; Petrakis & Moulet, 2011; Simov et al., 2017), Spain (Baena & Torres, 2012; Vivas, 2012), Italy (Pinzari et al., 2018), Turkey (Çerçi & Koçak, 2016) and Albania (van der Heyden, 2017). These studies suggest that this species could be a good candidate for biological control of *P. spumarius* in olive orchards

(Salerno et al., 2017), however *Z. renardii* is a zoophagous generalist (Pinzari et al., 2018) and the impacts of its introduction should be carefully evaluated.

4.3. Molecular analysis

The results of this study showed the absence of the bacterium in all the different tested spittlebugs species captured in the Alentejo olive groves. However, the presence of *X. fastidiosa* have been reported in north of Portugal and the ever-growing number of detections shows high probability of the phytopathogen reaching the Alentejo Region. Also, the sampling period for this study occurred in spring 2017, meaning that roughly three years have passed since then and almost two years since the first detection of *X. fastidiosa* in December 2018, to be sure that the bacterium did not reach the study area new molecular studies should be conducted on the spittlebugs populations in Alentejo olive groves, as well as further studies of their biology and ecology in the climate conditions of Portugal.

4.4. Contribution to the management strategy

As mentioned before, there is no treatment currently available to cure infected plants with *X. fastidiosa* and in absence of a cure, prevention or containment is the way to go. Since the bacterium has already been detected in Portugal, it is crucial that it does not reach the Alentejo Region, where several economically important crops are produced.

The adopted strategy to eradicate *X. fastidiosa* in Portugal, as per requirement of European Union, goes through establishing a demarcated area, consisting of an infected zone and a buffer surrounding area. The infected zone has to include all "infected plants that have been detected, the rest plants of the same species and origin, as well as those in its immediate proximity and the vegetables within a 50m radius around the infected plants" and the buffer zone to be of at least 2,5 km radius, surrounding the infected zone. If a new presence of bacteria is confirmed in the demarcated area, the boundary of the infected area and the buffer zone must be immediately revised and changed accordingly. An extensive and continuous monitoring plan should be devised to survey for the presence of *X. fastidiosa* by examining the health of plants and the presence of potential vectors. The infected plants found and all host plants of the bacterium, within a radius of 50m, should be destroyed on the spot, under official supervision. Any new detection of infection will imply the extension of application of these measures to a new 50 m radius around the new focus. Also, before the removal/destruction of the hosts, the insect vectors must be submitted to chemical control, biological or mechanical control. Propagation of plants that have been grown for at least part of their life cycle in the demarcated area may only move out of the demarcated area and infected areas into the buffer provided they are accompanied by a phytosanitary passport attesting to the compliance with the phytosanitary measures referred to in Decision EU / 789/2015 and amendments (DRE, 2020).

Considering the eradication strategy described above, olive trees, ground vegetation and vectors/potential vectors should be thoughtfully monitored in the Alentejo olive groves. The monitoring plan should focus mainly on the potential and vector species like *P. spumarius, P. tesselatus, N. campestris, C. intermedia* and *L. coleoptrata,* with the primary focus on the first three, since *P. spumarius* is a confirmed *X. fastidiosa* vector, since *P. tesselatus* was the most abundant species found in the study and since *N. campestris* transmission abilities have been verified.

Special attention should be payed to the surrounding ground vegetation, especially to plant families that contain plant species susceptible to *X. fastidiosa*. The results of this study show that plant families like Asteraceae, Apiaceae (*D. carota*, *C. maculatum*) and Convolvulaceae (*C. arvensis*) should be more closely monitored and if, the situation becomes critical, removed.

5. Conclusions

In conclusion, so far, *X. fastidiosa* has not been detected in the Alentejo Region, however the present survey demonstrated that in the Alentejo olive groves, five vector species were present, namely *P. spumarius*, *P. tesselatus*, *C. intermedia*, *L. coleoptrata* and *N. campestris*. The monitoring plan should focus on *P. tesselatus*, as it was the most abundant species found, *P. spumarius*, as it is a confirmed *X. fastidiosa* vector and *N. campestris*, as it represents a treat if the phytopathogen reaches the region, not only to olive trees but to the surrounding cultures, as its transmission abilities have been verified.

A clear difference in aedeagus morphology between *P. spumarius* and *P. tesselatus* was found in this study and being able to correctly identify the specie is very important as it is directly related to the establishment of efficient control practices of the insect vectors and disease management, in accordance to their ecological preferences.

Several other Auchenorrhyncha species that are known vectors to other diseases were captured. Two individuals of *Arocephalus punctum* were found in this study and to the author's knowledge, this may be the first report of this leafhopper in Portugal.

No difference was observed in host plant preference by the vectors, except for the *Philaenus* sp., which showed higher abundance on ground cover that on olive trees. Nevertheless, the herbaceous vegetation present in the region should also be subjected to prospection and, if the situation becomes critical, should be removed. Special attention must be payed to the plant families were the insect vectors found were most abundant or to the families that are vulnerable to the bacterium, specially Asteraceae, Apiaceae and Convolvulaceae.

Further studies should be conducted to verify if the Dryinidae can, in fact, parasitize spittlebugs as well as, studies to identify natural enemies of vectors in Alentejo olive groves, their ecological relations and if the management of the natural enemies could contribute to biological control of *X. fastidiosa* vectors.

Finally, it was shown that, in the study area, temperature and precipitation play a significant role in abundance of *Philaenus* spp. This means that future climate change could impact the epidemiology of olive quick decline syndrome in Alentejo olive orchards, since climatic variables can influence the distribution and dynamics of vector populations, host plants growth, the efficiency of pathogen transmission and vector/host plant dynamics.

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Annex A – Meteorological data

Table A.1 – Mensal minimum temperature (°C) data from IPMA climatological stations in Portugal in 2017.

Climatological station	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec
Aveiro	5.7	8.5	9.5	12.3	14.4	16.5	16.8	16.4	14.0	13.2	9.3	6.8
Beja	4.3	7.3	7.8	10.0	13.1	15.8	15.5	16.2	13.5	15.5	9.3	5.8
Braga	1.3	5.4	5.8	7.3	11.6	13.7	14.1	13.4	10.1	8.5	3.7	2.9
Bragança	-1.2	3.0	3.9	5.6	10.3	14.3	13.9	14.0	9.7	7.5	1.0	0.6
Castelo Branco	3.5	6.3	6.8	10.2	13.0	16.7	17.2	17.8	14.9	14.7	8.0	5.1
Coimbra	3.2	6.8	8.0	9.8	12.3	14.3	14.8	14.1	11.3	10.6	6.2	4.1
Évora	2.9	6.5	6.4	8.7	12.1	15.4	15.5	15.9	13.6	13.4	7.8	4.4
Faro	7.6	10.7	11.1	14.0	16.4	20.7	20.2	20.8	18.3	18.0	12.8	8.8
Guarda	0.6	2.6	3.8	6.8	9.8	13.8	13.5	13.8	11.1	12.6	5.2	2.5
Leiria	2.2	6.6	7.8	8.5	12.4	14.6	14.9	14.2	11.2	10.2	5.8	3.8
Lisboa	7.1	9.7	10.1	12.9	14.6	17.3	17.3	17.7	15.9	15.7	10.7	7.9
Portalegre	5.2	6.8	7.3	11.6	13.2	16.6	17.2	17.6	15.9	17.1	10.0	6.3
Portimão	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Porto - Pedras Rubras	5.5	8.3	9.2	10.9	13.2	15.1	15.7	15.8	12.6	12.7	8.5	6.9
Porto - Serra do Pilar	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Santarém	4.8	8.2	8.9	10.9	13.2	15.8	16.1	16.1	13.7	14.0	9.0	6.2
Setúbal	3.8	6.5	7.4	8.8	12.4	15.6	16.3	16.0	14.5	12.2	8.0	4.3
Viana do Castelo	4.0	6.8	7.6	9.2	12.4	13.2	14.8	14.3	11.5	10.3	6.9	5.3
Vila Real	2.0	5.2	5.8	8.3	11.5	14.6	14.7	14.8	11.6	12.1	5.5	3.5
Viseu	2.7	4.7	5.8	8.4	10.5	13.7	13.8	13.7	11.3	13.3	6.6	3.8

Table A.2 – Mensal mean temperature (°C) data from IPMA climatological stations in Portugal in 2017.

Climatological station	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec
Aveiro	10.2	13.0	14.0	17.2	18.7	20.1	20.4	20.6	18.2	19.1	14.0	11.4
Beja	9.1	11.7	13.3	17.3	20.2	24.4	25.2	25.4	22.2	22.3	14.8	10.5
Braga	7.9	11.1	12.1	15.4	18.2	21.0	21.4	21.5	18.1	17.8	11.2	9.0
Bragança	4.5	8.0	10.0	13.6	16.8	22.1	22.6	22.4	18.1	16.1	8.1	5.7
Castelo Branco	8.0	10.8	12.3	16.7	19.2	24.6	25.7	26.0	22.6	21.1	12.9	9.5
Coimbra	9.2	12.2	13.7	17.3	19.0	21.3	21.7	22.3	19.4	19.6	13.1	10.0
Évora	8.6	11.5	12.6	16.6	19.8	24.5	25.2	25.4	22.3	21.5	14.0	9.8
Faro	12.0	13.9	13.9	17.9	20.3	25.2	25.2	25.4	22.7	22.1	16.9	13.1
Guarda	4.0	6.4	8.2	12.5	14.8	20.2	20.5	20.8	17.4	17.4	8.7	5.7
Leiria	8.5	11.8	13.2	16.5	18.5	20.3	20.3	20.6	17.8	18.6	12.4	9.7
Lisboa	10.7	13.0	14.3	18.2	19.7	22.9	22.9	23.6	21.5	21.4	14.8	11.6
Portalegre	8.3	10.3	11.8	16.9	18.9	23.9	24.8	25.2	22.3	21.7	13.7	9.3
Portimão	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Porto - Pedras Rubras	9.9	12.2	13.3	13.7	18.6	22.8	21.0	21.5	18.0	19.0	13.7	11.1
Porto - Serra do Pilar	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Santarém	9.9	13.0	14.4	18.5	20.3	23.8	24.0	24.6	22.0	22.2	14.7	11.3
Setúbal	9.7	12.2	13.6	17.1	19.6	23.5	23.9	24.0	22.1	20.8	14.5	10.7
Viana do Castelo	8.5	11.3	12.7	15.1	17.3	18.5	19.7	19.7	16.9	16.8	11.9	9.6
Vila Real	6.1	9.4	11.0	15.1	17.6	21.5	22.2	22.6	18.9	18.8	10.5	7.4
Viseu	7.0	9.1	10.7	15.0	16.5	20.9	21.7	22.1	18.9	19.6	11.6	7.8

Table A.3 – Mensal maximum temperature (°C) data from IPMA climatological stations in Portugal in 2017.

Climatological station	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec
Aveiro	14.7	17.4	18.4	22.1	23.1	23.8	23.9	24.7	22.3	25.0	18.7	16.0
Beja	13.9	16.0	18.8	24.6	27.2	33.1	34.8	34.6	30.8	29.1	20.3	15.1
Braga	14.5	16.8	18.4	23.6	24.7	28.4	28.7	29.6	26.2	27.2	18.8	15.0
Bragança	10.2	12.9	16.1	21.6	23.4	29.8	31.3	30.9	26.5	24.7	15.3	10.7
Castelo Branco	12.5	15.2	17.8	23.2	25.4	32.6	34.1	34.1	30.3	27.5	17.8	13.9
Coimbra	15.2	17.6	19.3	24.8	25.7	28.3	28.6	30.5	27.5	28.6	20.0	15.9
Évora	14.3	16.4	18.8	24.6	27.5	33.5	34.9	35.0	31.0	29.5	20.1	15.1
Faro	16.4	17.0	19.0	21.9	24.1	29.7	30.2	29.9	27.2	26.2	21.0	17.3
Guarda	7.3	10.1	12.5	18.2	19.9	26.7	27.6	27.8	23.7	22.1	12.3	8.8
Leiria	14.8	17.0	18.5	24.4	24.6	26.0	25.8	27.0	24.5	27.0	19.0	15.5
Lisboa	14.2	16.3	18.4	23.6	24.7	28.5	28.5	29.5	27.2	27.1	18.8	15.2
Portalegre	11.5	13.8	16.3	22.2	24.6	31.1	32.5	32.8	28.7	26.4	17.4	12.3
Portimão	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Porto - Pedras Rubras	14.3	16.1	17.4	16.5	23.9	30.4	26.2	27.1	23.4	25.2	18.9	15.2
Porto – Serra do Pilar	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Santarém	15.0	17.8	19.9	26.0	27.5	31.8	31.9	33.2	30.2	30.3	20.5	16.4
Setúbal	15.6	17.9	19.8	25.4	26.8	31.4	31.5	32.0	29.7	29.4	21.0	17.0
Viana do Castelo	13.0	15.8	17.8	21.1	22.1	23.8	24.5	25.2	22.4	23.3	16.9	13.8
Vila Real	10.2	13.5	16.2	22.0	23.7	28.5	29.6	30.4	26.2	25.4	15.6	11.3
Viseu	11.4	13.5	15.6	21.7	22.5	28.2	29.5	30.5	26.6	25.9	16.5	11.8

Table A.4 – Mensal total precipitation (mm) data from IPMA climatological stations in Portugal in 2017.

Climatological station	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec
Aveiro	108.1	119.2	131.3	26.8	112.3	1.2	0.6	4.7	5.5	39.5	NA	128.9
Beja	65.3	61.2	83.5	4.8	16.9	3.4	0.0	21.8	0.0	18.0	63.9	40.4
Braga	NA	NA	NA	NA	170.4	30.8	23.3	8.2	9.5	59.7	113.7	NA
Bragança	46.2	173.0	49.0	15.9	74.4	5.8	6.6	5.3	0.0	17.2	45.3	116.2
Castelo Branco	44.3	101.9	69.7	5.4	49.8	13.2	3.8	4.8	0.0	16.6	68.3	41.7
Coimbra	49.3	79.9	85.5	13.0	73.8	8.0	6.4	32.3	4.2	27.8	59.7	107.3
Évora	39.3	50.0	77.8	0.6	43.9	8.2	0.0	16.9	0.0	21.1	45.1	44.8
Faro	30.2	82.9	78.4	21.2	25.0	NA	0.0	NA	0.0	7.4	27.5	39.9
Guarda	55.0	178.0	67.1	17.5	74.7	3.1	0.1	4.5	0.1	22.7	88.2	91.2
Leiria	NA	NA	NA	NA	38.3	22.4	3.2	1.0	3.6	NA	67.9	92.4
Lisboa	84.7	77.2	97.8	4.7	59.1	0.4	1.2	9.5	0.0	31.5	70.3	54.2
Portalegre	54.5	85.5	80.3	3.1	82.0	2.6	0.0	NA	0.0	19.2	NA	69.7
Portimão	NA	NA	NA	NA	NA	4.6	NA	NA	NA	NA	NA	NA
Porto - Pedras Rubras	100.9	162.6	116.0	NA	110.0	20.0	4.3	2.2	NA	NA	NA	162.8
Porto - Serra do Pilar	NA	NA	NA	26.0	NA	NA	NA	NA	NA	NA	NA	NA
Santarém	93.5	35.8	60.5	3.0	58.6	0.5	1.2	10.5	0.3	25.4	NA	46.1
Setúbal	53.8	71.2	89.1	2.0	71.7	4.4	0.0	0.1	0.0	15.7	41.3	46.9
Viana do Castelo	103.1	169.8	101.9	10.5	101.4	25.0	13.6	6.7	8.4	63.0	79.8	154.5
Vila Real	62.9	168.7	61.2	11.2	79.8	11.0	20.4	2.3	0.1	29.5	32.2	157.7
Viseu	77.6	181.8	93.7	17.4	101.5	17.8	10.9	26.7	1.2	45.5	63.8	167.5

Table A.5 – Characterization of the climatological stations from which mensal meteorological data was acquired. ACS - Automatic Climatological Station; APS - Automatic Principal Station; AUS – Automatic Urban Station.

Climatological station	Code	Type	Latitude (º)	Longitude (º)	Altitude (m)
Aveiro / Universidade	702	ACS	40.63540000	-8.65961111	5
Beja	562	EAP	38.02572778	-7.86731944	246
Braga - Merelim	622	ACS	41.57586944	-8.45110833	65
Bragança	575	EAP	41.80388333	-6.74283056	690
Castelo Branco	570	EAP	39.83944444	-7.47869444	386
Coimbra - Bencanta	707	ACS	40.21346944	-8.45515278	35
Évora / Aeródromo	558	EAP	38.53654167	-7.88795833	246
Faro / Aeroporto	554	EAP	37.01657778	-7.97195278	8
Guarda	683	ACS	40.52855833	-7.27867500	1020
Leiria / Aeródromo	718	ACS	39.78055278	-8.82096667	45
Lisboa /Gago Coutinho	579	EAP	38.76620278	-9.12749444	104
Portalegre	571	EAP	39.29418333	-7.42131667	597
Portimão / Aeródromo	878	ACS	37.14748056	-8.58328333	2
Porto - Pedras Rubras	545	EAP	41.23227500	-8.67910833	69
Porto - Serra do Pilar	546	EAU	41.13851944	-8.60250000	93
Santarém - Fonte Boa / Est. Zootécnica	734	ACS	39.20126111	-8.73666111	73
Setúbal / Estação de Fruticultura	770	ACS	38.54849722	-8.89078333	35
Viana do Castelo - Chafé	551	EAP	41.64887500	-8.80460556	48
Vila Real / Cidade	566	EAU	41.30898056	-7.74052222	481
Viseu / Cidade	675	EAU	40.66273889	-7.90396944	443

Annex B – Distribution of geographical units in Alentejo Region

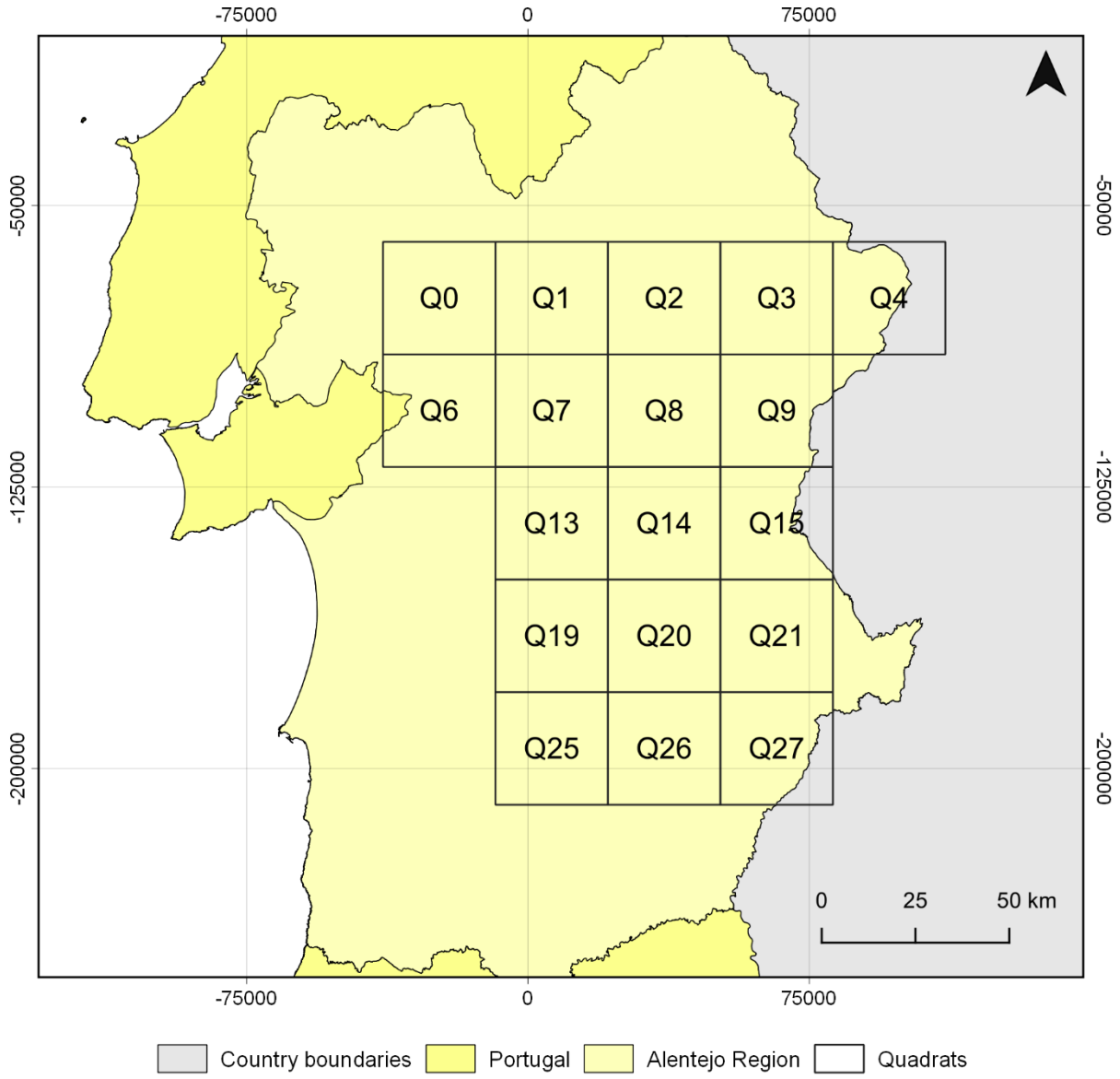

Figure B. 1 – Distribution of 18 geographical units (GUs) of 30 × 30 km in which the Alentejo Region was divided for sampling. Map projected in ETRS89/TM06-PT.

Annex C – Metadata

Table C.1 – Metadata associated with the data used in this dissertation.

Data	Source	Metadata	Site
Administrative limits of world countries	Geoportal of European Commission (Eurostat)	**Format**: Shapefile (shp); **Coordinate reference system:** WGS84; **Reference period:** 2016; **Datum:** World Geodetic System 1984; **Ellipsoid:** WGS84; **Spatial resolution:** 1:1 Million	https://ec.europa.eu/eurostat/web/gisco/geodata/reference-data/administrative-units-statistical-units/countries#countries14
Administrative limits of Portugal	Direção Geral do Território (DGT)	**Format**: Shapefile (shp); **Coordinate reference system:** ETRS89/PT-TM06; **Reference period:** 2017; **Datum:** ETRS89; **Ellipsoid:** GRS80; **Spatial resolution:** 1:25 000m	http://www.dgterritorio.pt/cartografia_e_geodesia/cartografia/carta_administrativa_oficial_de_portugal_caop/caop__download_/carta_administrativa_oficial_de_portugal___versao_2017/
Digital elevation model	Personal page of Professor José Alberto Gonçalves (Universidade do Porto)	**Format:** Geotiff; **Coordinate reference system:** WGS84; **Spatial resolution:** 1 s	http://www.fc.up.pt/pessoas/jagoncal/srtm/
Water and Wetness	Copernicus Land Monitoring Service	**Format**: Geotiff; **Coordinate reference system:** ETRS89, LAEA; **Reference period:** 2015; **Spatial resolution:** 20 m	https://land.copernicus.eu/pan-european/high-resolution-layers/water-wetness/status-maps/2015

Annex D – Auchenorrhyncha habitus and genital characters

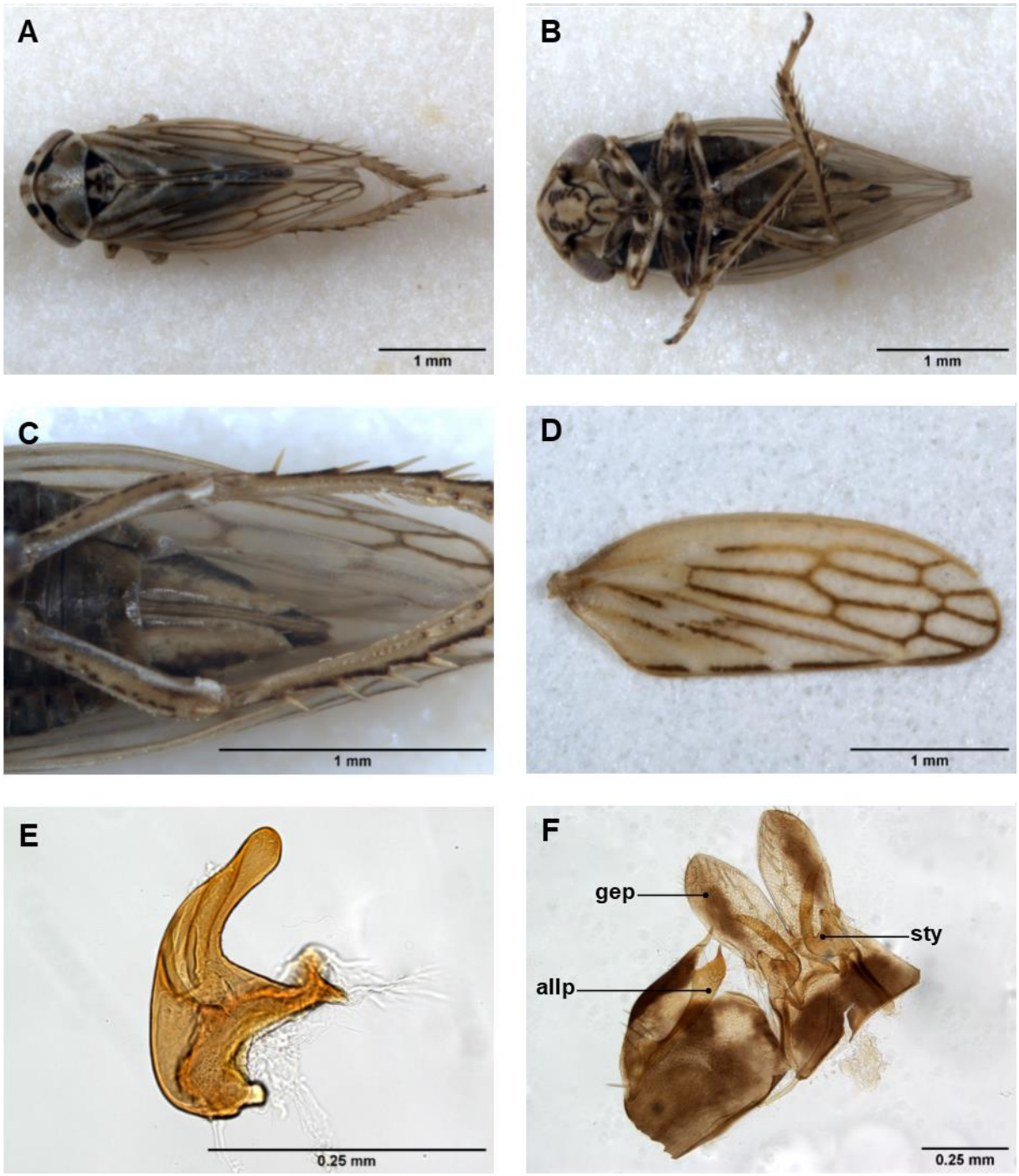

Figure D. 1 – Morphological aspects of *Agallia consobrina* Curtis. **A** – Dorsal view. **B** – Ventral view. **C** – Detail of female genitalia in ventral view. **D** – Forewing. **E** – Aedeagus. **F** – Anal tube. aed = aedeagus; allp = appendages of lateral lobe of pygofer; ast = anal style; atu = anal tube; con = connective; gep = genital plates; lowap = lower appendages of aedeagus; midap = middle appendages of aedeagus; pyg = pygofer; sty = styles; sym = sympodite; uppap = upper appendages of aedeagus.

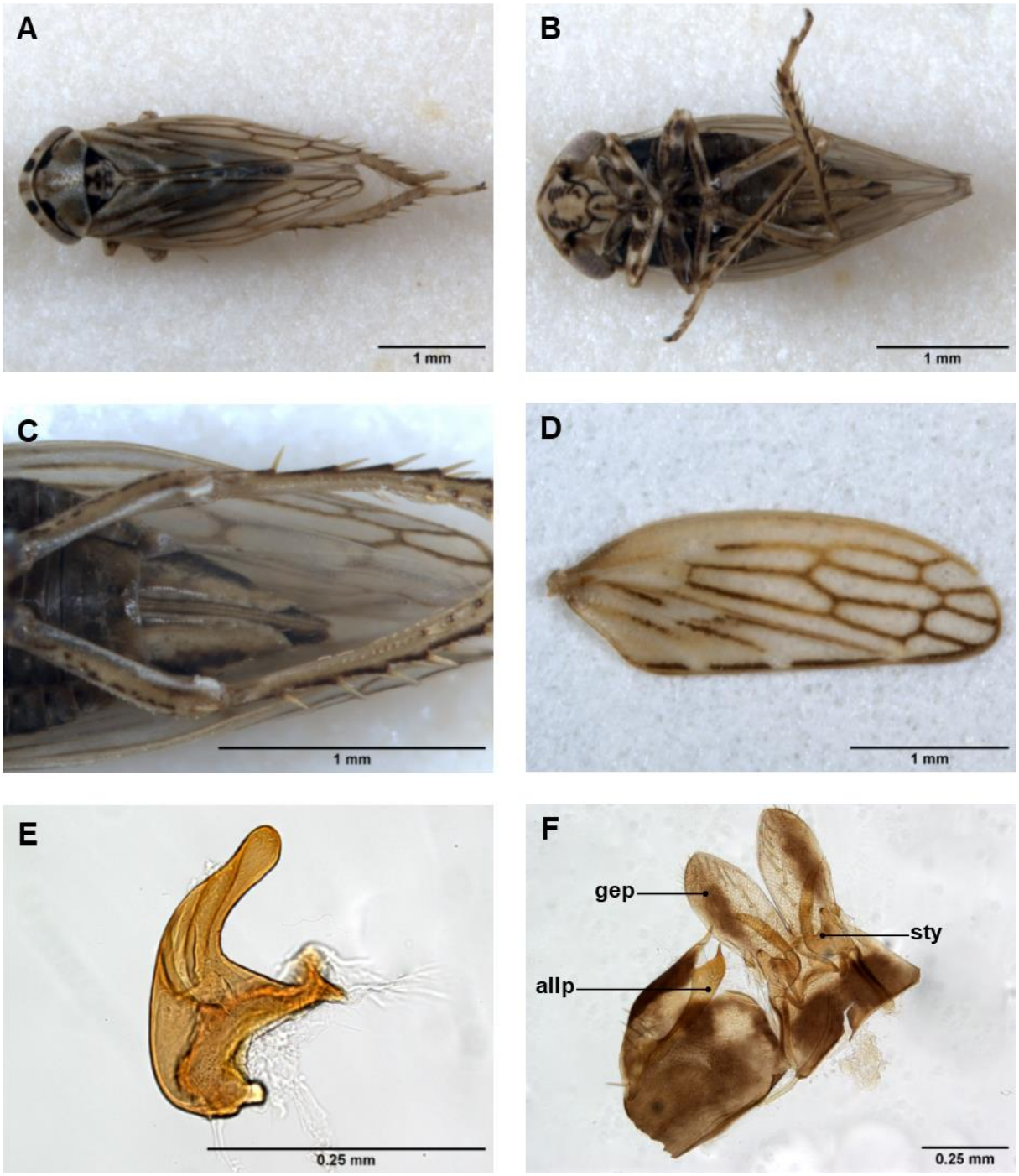

Figure D. 2 – Morphological aspects of *Anaceratagallia laevis* (Ribaut). **A** – Dorsal view. **B** – Ventral view. **C** – Detail of female genitalia in ventral view. **D** – Forewing. **E** – Aedeagus. **F** – Male genital capsule. aed = aedeagus; allp = appendages of lateral lobe of pygofer; ast = anal style; atu = anal tube; con = connective; gep = genital plates; lowap = lower appendages of aedeagus; midap = middle appendages of aedeagus; pyg = pygofer; sty = styles; sym = sympodite; uppap = upper appendages of aedeagus.

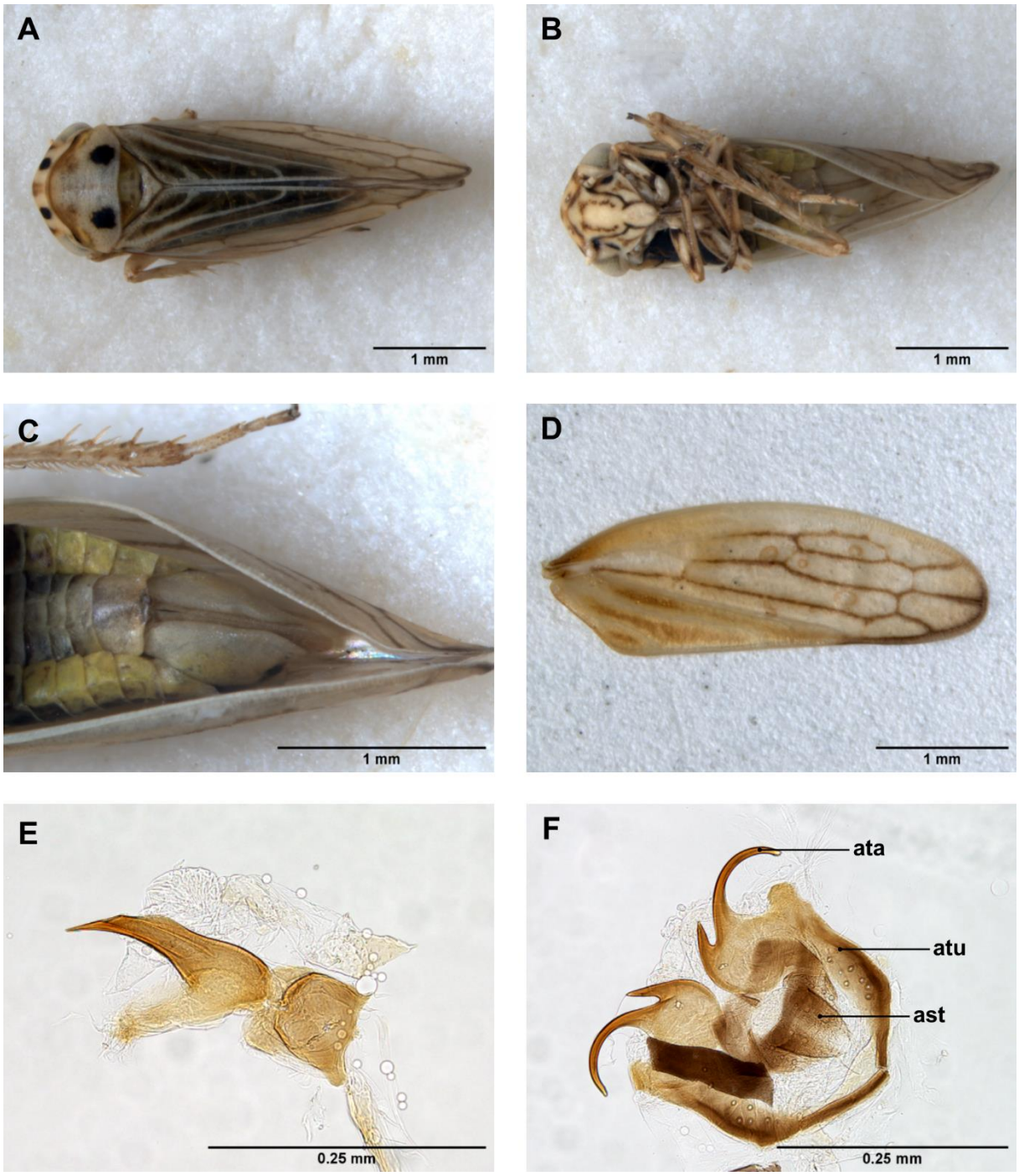

Figure D. 3 – Morphological aspects of *Austroagallia sinuata* (Mulsant & Rey). **A** – Dorsal view. **B** – Ventral view. **C** – Detail of female genitalia in ventral view. **D** – Forewing. **E** – Aedeagus. **F** – Male genital capsule. aed = aedeagus; allp = appendages of lateral lobe of pygofer; ast = anal style; atu = anal tube; con = connective; gep = genital plates; lowap = lower appendages of aedeagus; midap = middle appendages of aedeagus; pyg = pygofer; sty = styles; sym = sympodite; uppap = upper appendages of aedeagus.

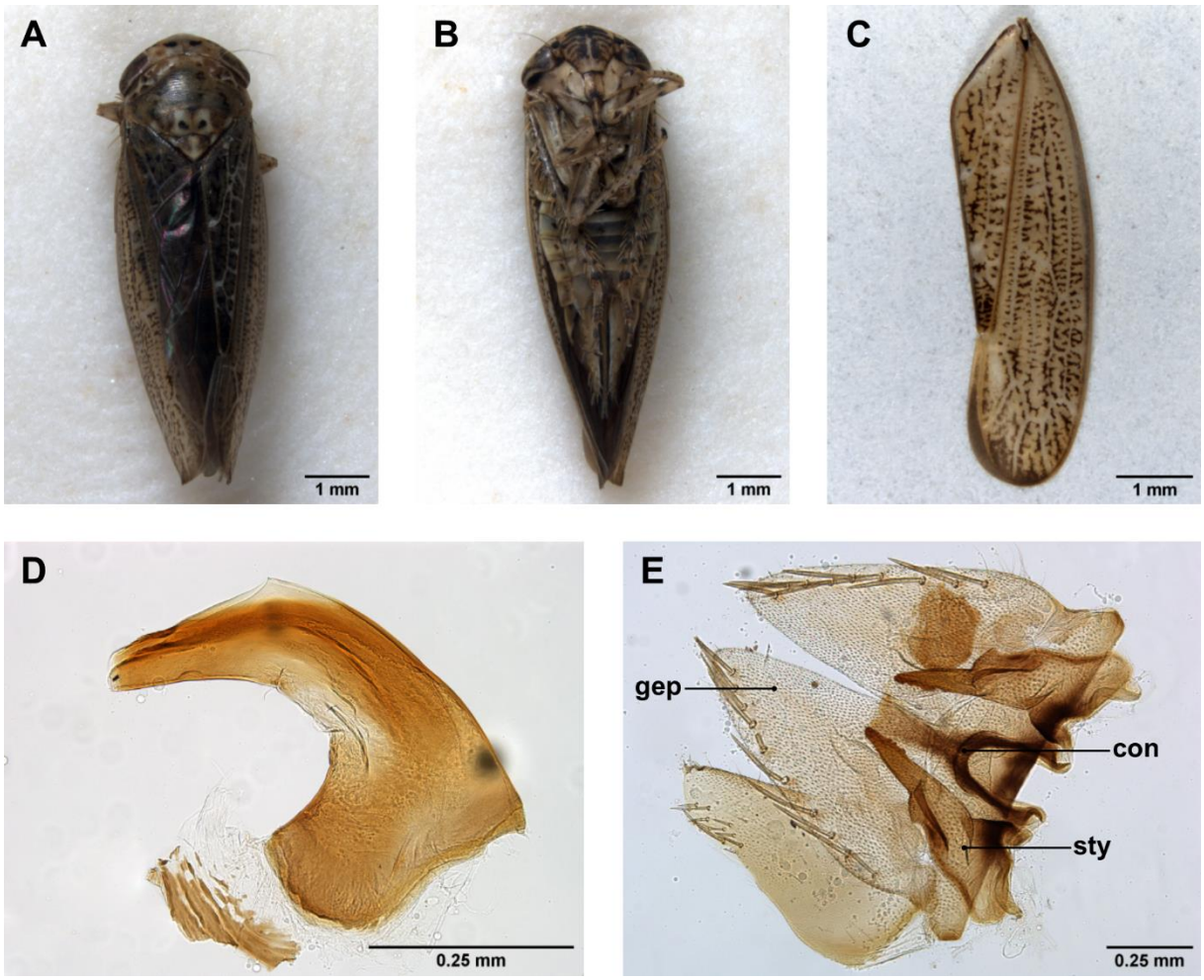

Figure D. 4 – Morphological aspects of *Allygus provincialis* (Ferrari). **A** – Dorsal view. **B** – Ventral view. **C** – Forewing. **D** – Aedeagus. **E** – Male genital capsule. aed = aedeagus; allp = appendages of lateral lobe of pygofer; ast = anal style; atu = anal tube; con = connective; gep = genital plates; lowap = lower appendages of aedeagus; midap = middle appendages of aedeagus; pyg = pygofer; sty = styles; sym = sympodite; uppap = upper appendages of aedeagus.

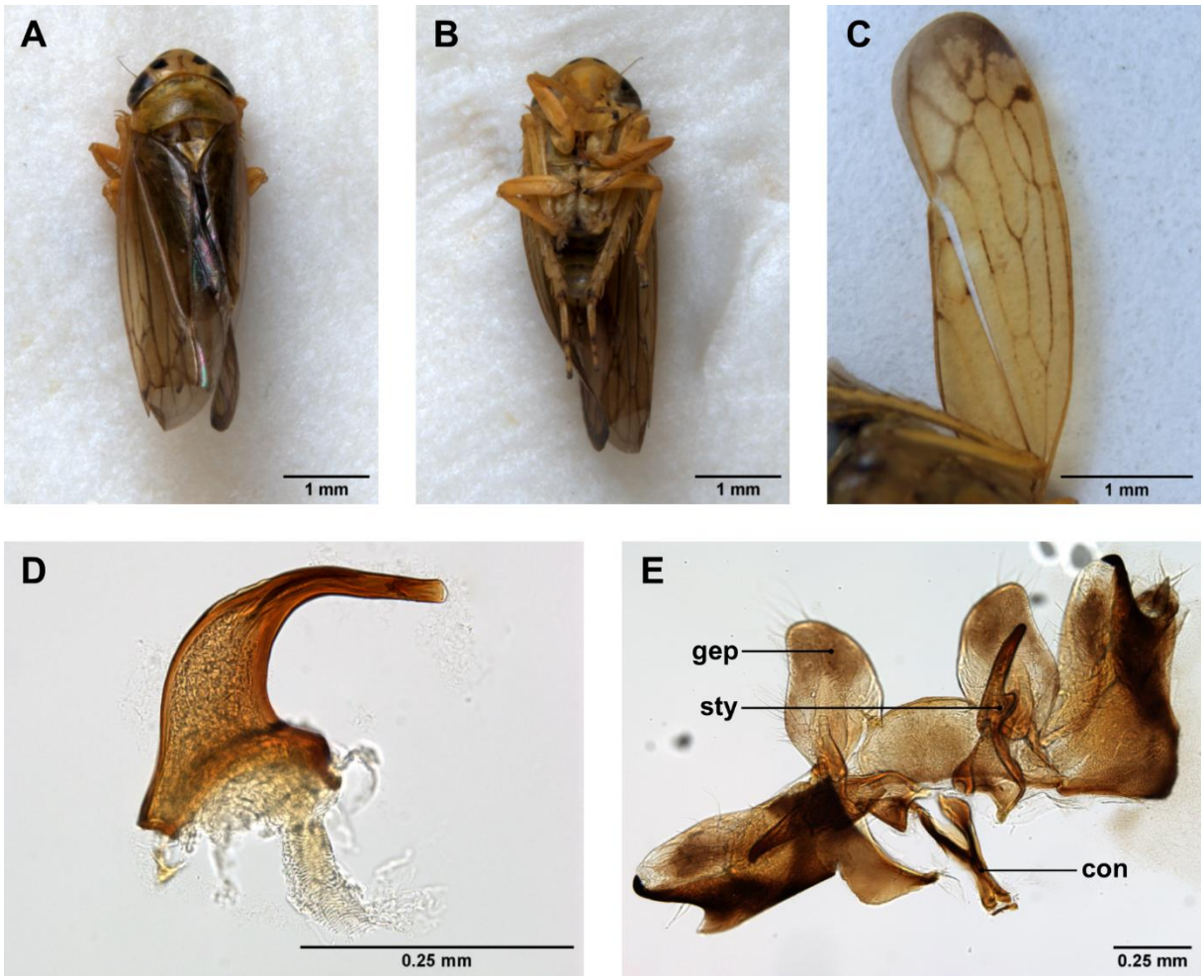

Figure D. 5 – Morphological aspects of *Anoplotettix ibericus* Remane. **A** – Dorsal view. **B** – Ventral view. **C** – Forewing. **D** – Aedeagus. **E** – Male genital capsule. aed = aedeagus; allp = appendages of lateral lobe of pygofer; ast = anal style; atu = anal tube; con = connective; gep = genital plates; lowap = lower appendages of aedeagus; midap = middle appendages of aedeagus; pyg = pygofer; sty = styles; sym = sympodite; uppap = upper appendages of aedeagus.

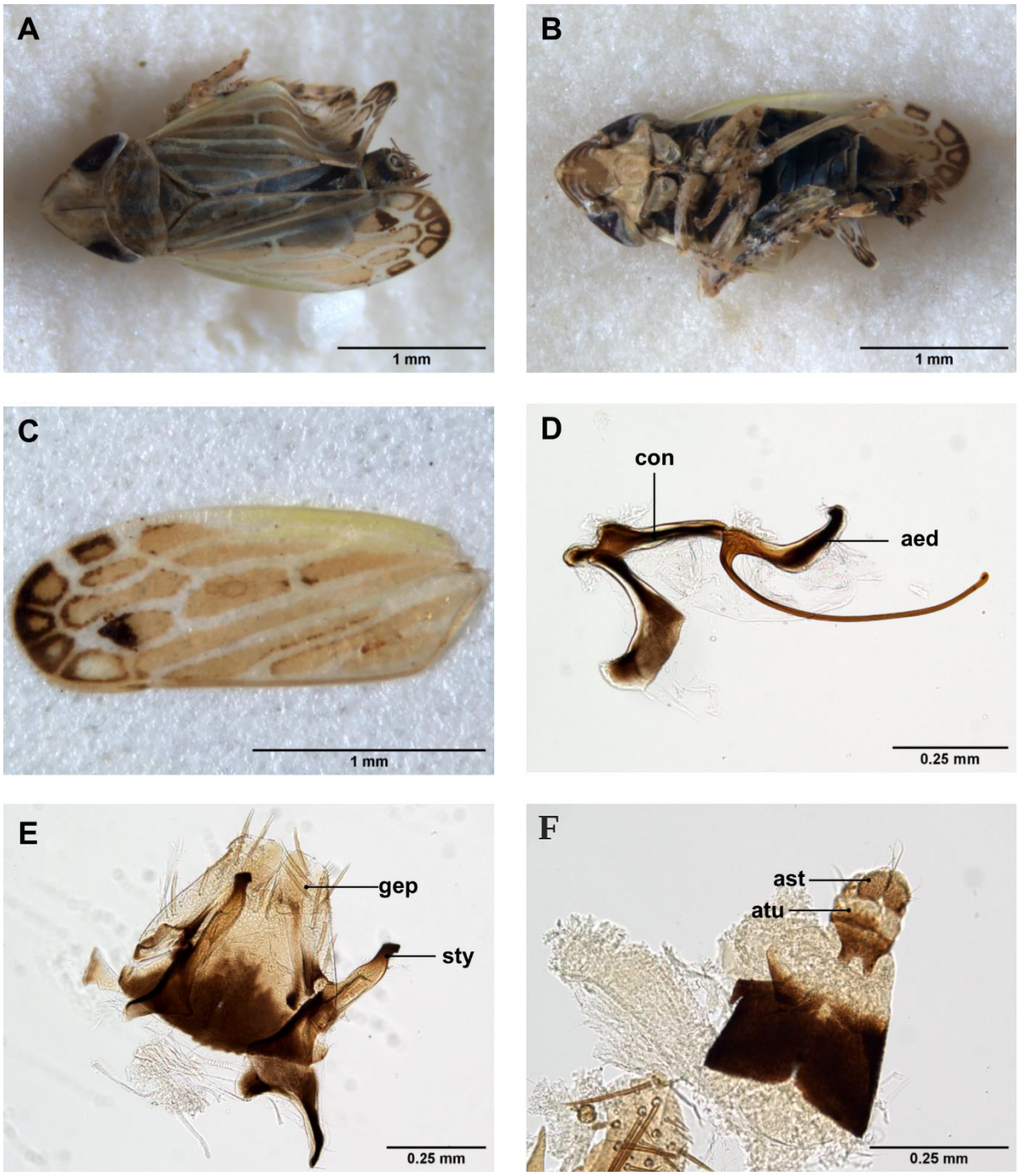

Figure D. 6 – Morphological aspects of *Arocephalus punctum (*Flor). **A** – Dorsal view. **B** – Ventral view. **C** – Forewing. **D** – Aedeagus and connective. **E** – Genital plates and styles. **F** – Anal tube and anal style. aed = aedeagus; allp = appendages of lateral lobe of pygofer; ast = anal style; atu = anal tube; con = connective; gep = genital plates; lowap = lower appendages of aedeagus; midap = middle appendages of aedeagus; pyg = pygofer; sty = styles; sym = sympodite; uppap = upper appendages of aedeagus.

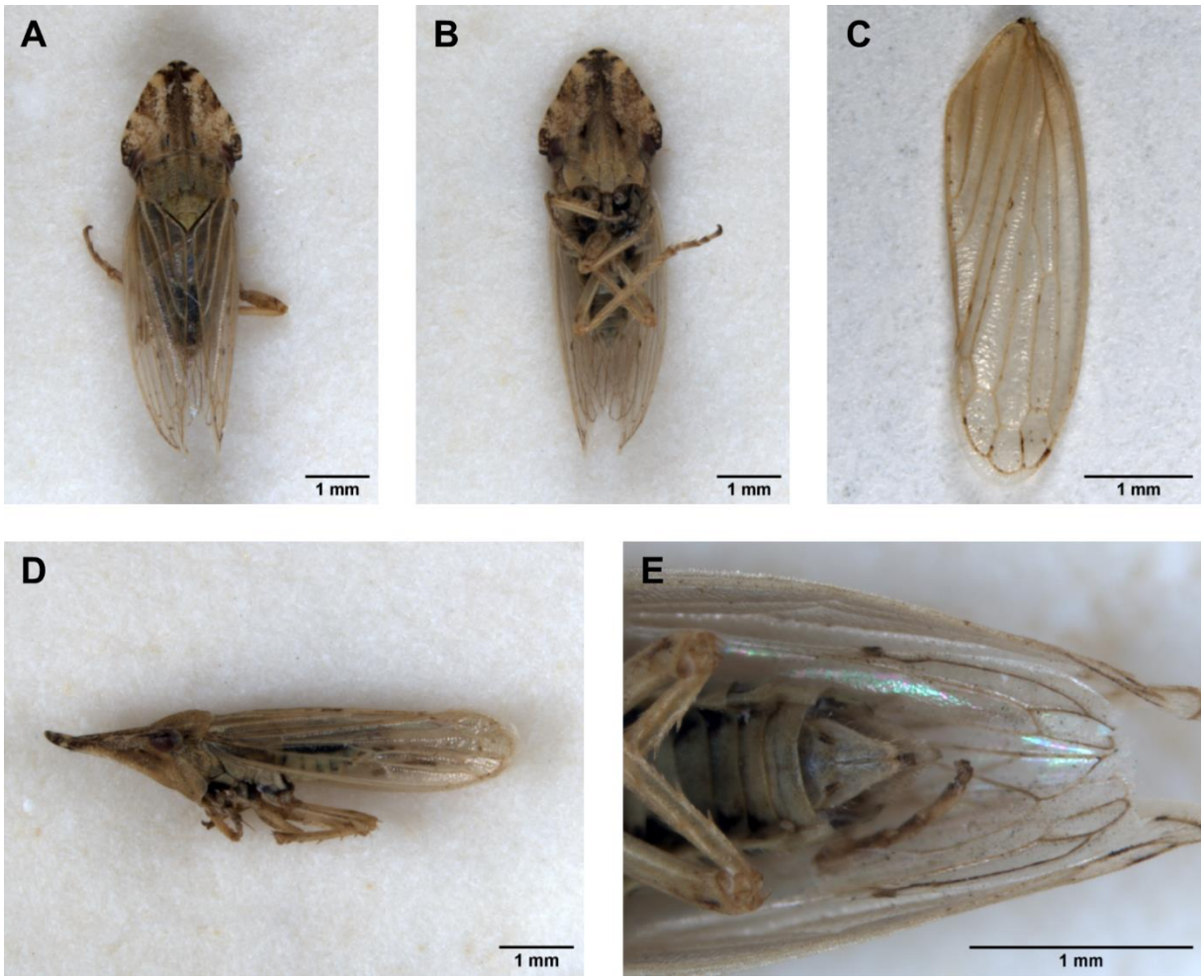

Figure D. 7 – Morphological aspects of *Eupelix cuspidata* (Fabricius). **A** – Dorsal view. **B** – Ventral view. **C** – Forewing. **D** – Lateral view. **E** – Detail of male genitalia in ventral view.

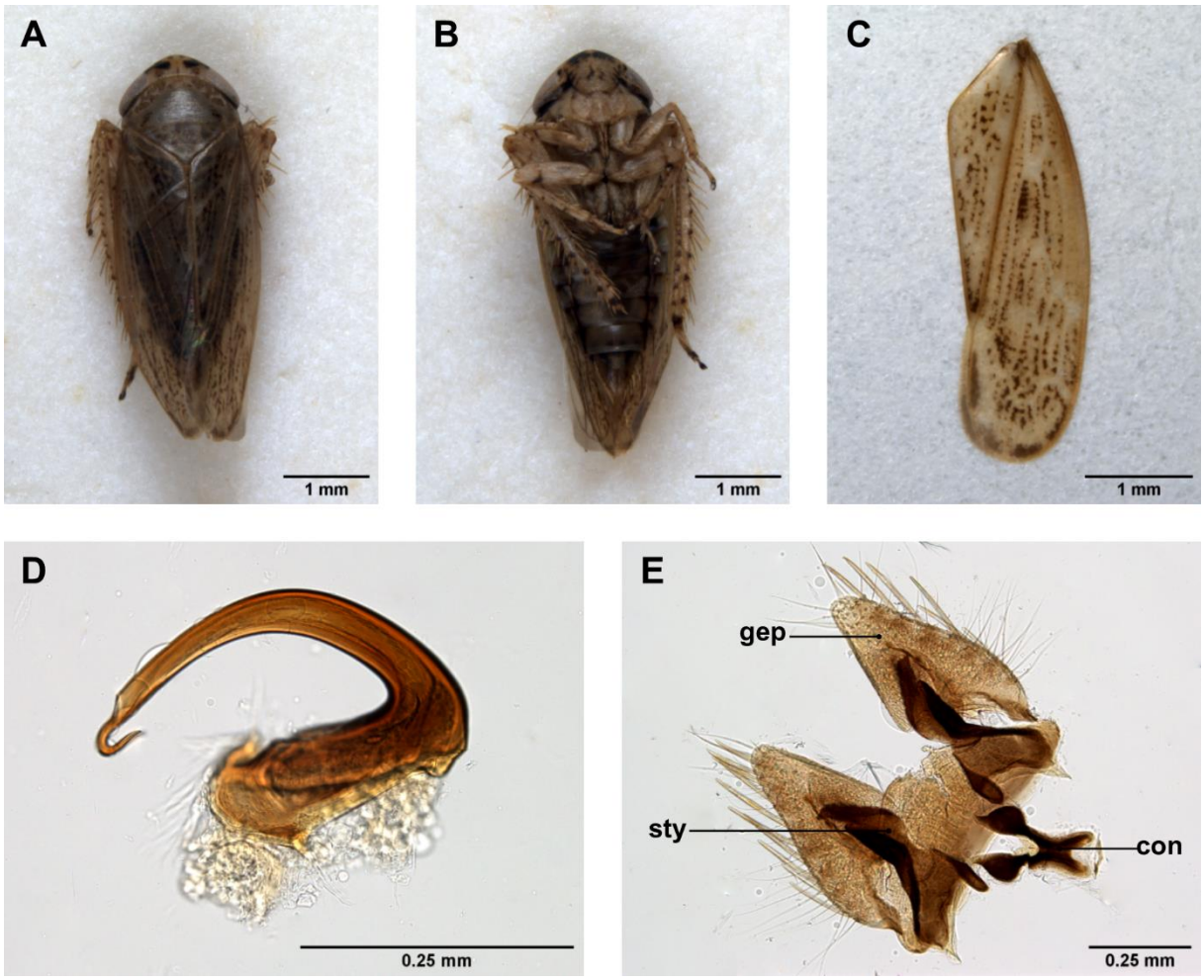

Figure D. 8 – Morphological aspects of *Euscelidius variegatus* (Kirschbaum). **A** – Dorsal view. **B** – Ventral view. **C** – Forewing**. D** – Aedeagus. **E** – Male genital capsule. aed = aedeagus; allp = appendages of lateral lobe of pygofer; ast = anal style; atu = anal tube; con = connective; gep = genital plates; lowap = lower appendages of aedeagus; midap = middle appendages of aedeagus; pyg = pygofer; sty = styles; sym = sympodite; uppap = upper appendages of aedeagus.

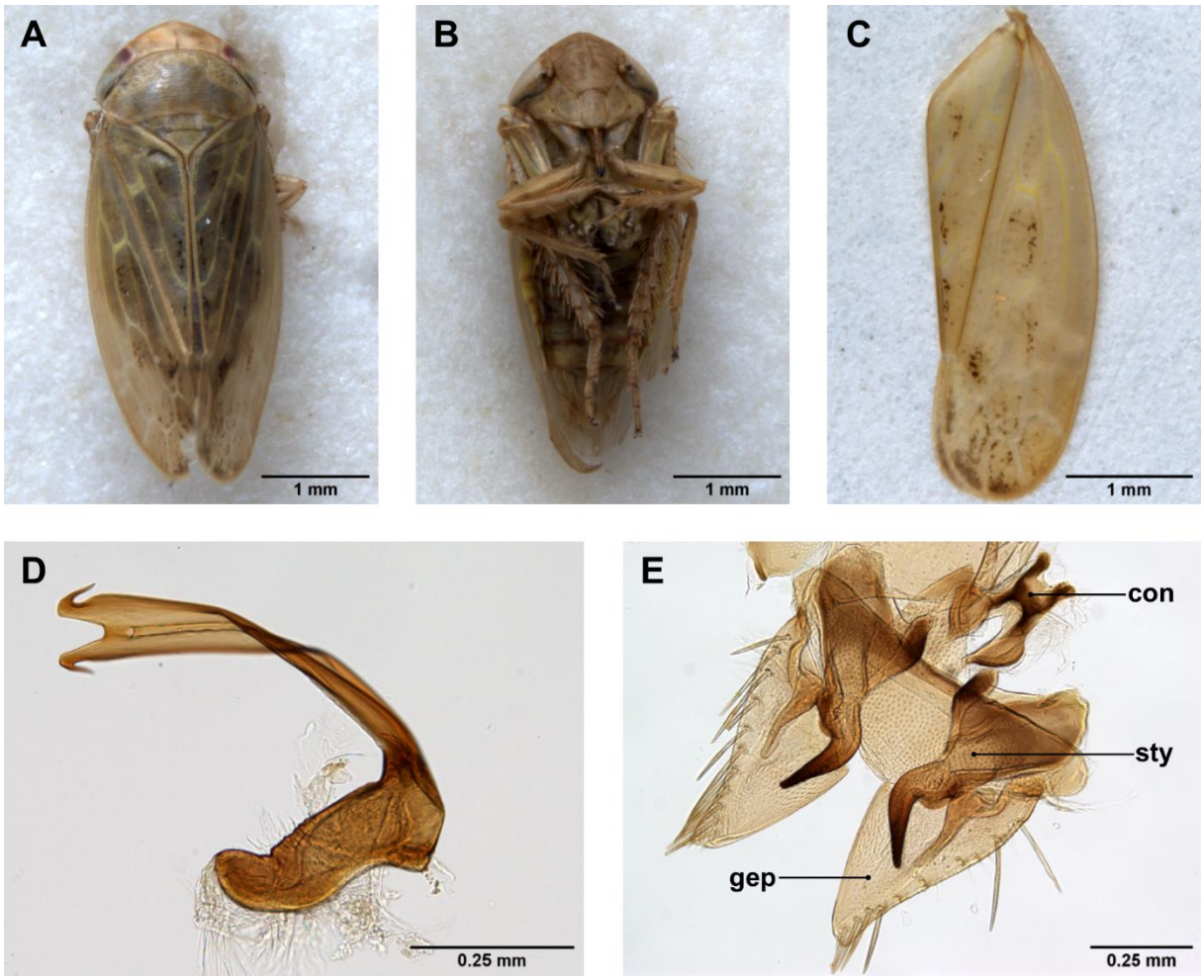

Figure D. 9 – Morphological aspects of *Euscelis alsius* Ribaut. **A** – Dorsal view. **B** – Ventral view. **C** – Forewing**. D** – Aedeagus. **E** – Male genital capsule. aed = aedeagus; allp = appendages of lateral lobe of pygofer; ast = anal style; atu = anal tube; con = connective; gep = genital plates; lowap = lower appendages of aedeagus; midap = middle appendages of aedeagus; pyg = pygofer; sty = styles; sym = sympodite; uppap = upper appendages of aedeagus.

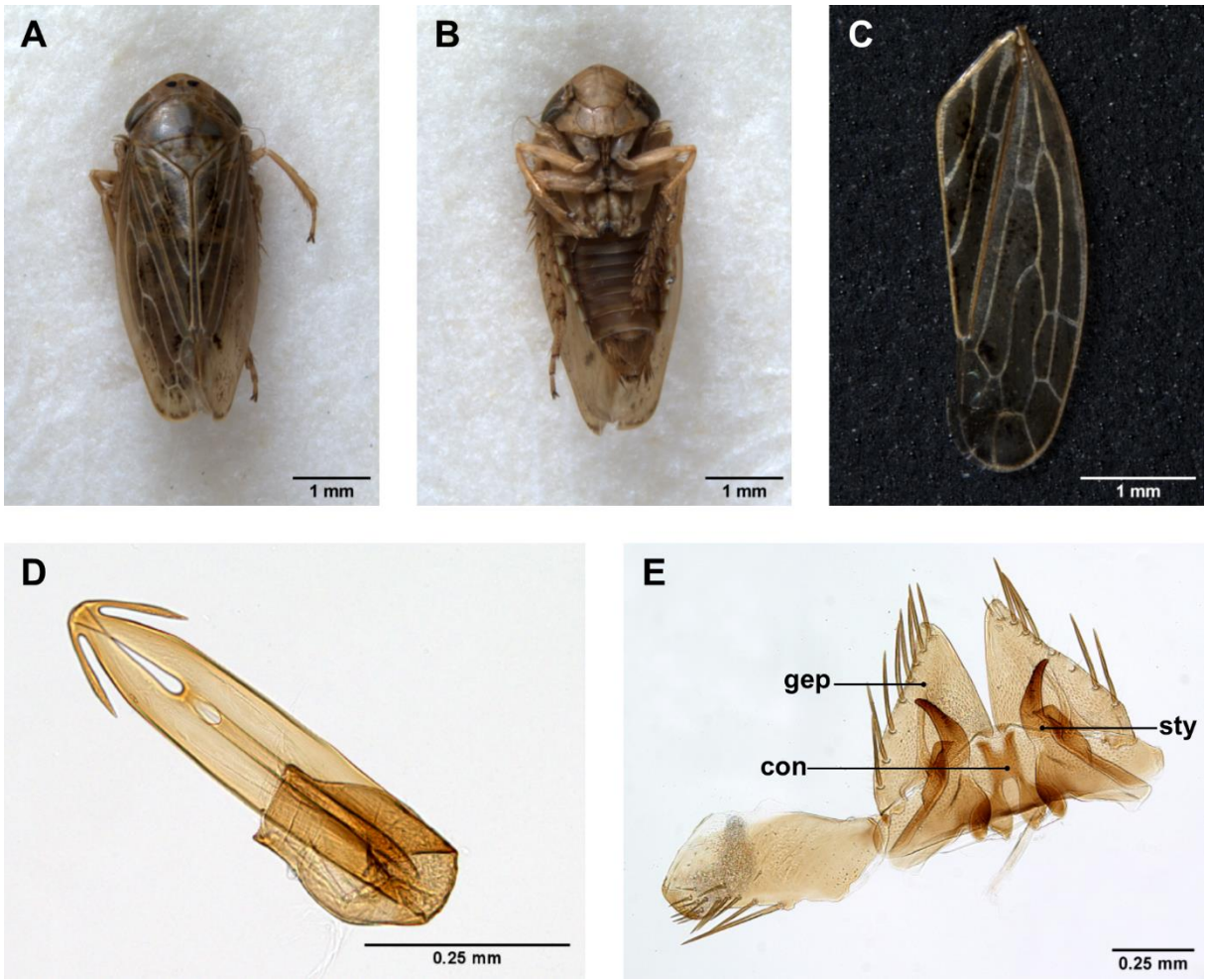

Figure D. 10 – Morphological aspects of *Euscelis distinguendus* Kirschbaum. **A** – Dorsal view. **B** – Ventral view. **C** – Forewing**. D** – Aedeagus. **E** – Male genital capsule. aed = aedeagus; allp = appendages of lateral lobe of pygofer; ast = anal style; atu = anal tube; con = connective; gep = genital plates; lowap = lower appendages of aedeagus; midap = middle appendages of aedeagus; pyg = pygofer; sty = styles; sym = sympodite; uppap = upper appendages of aedeagus.

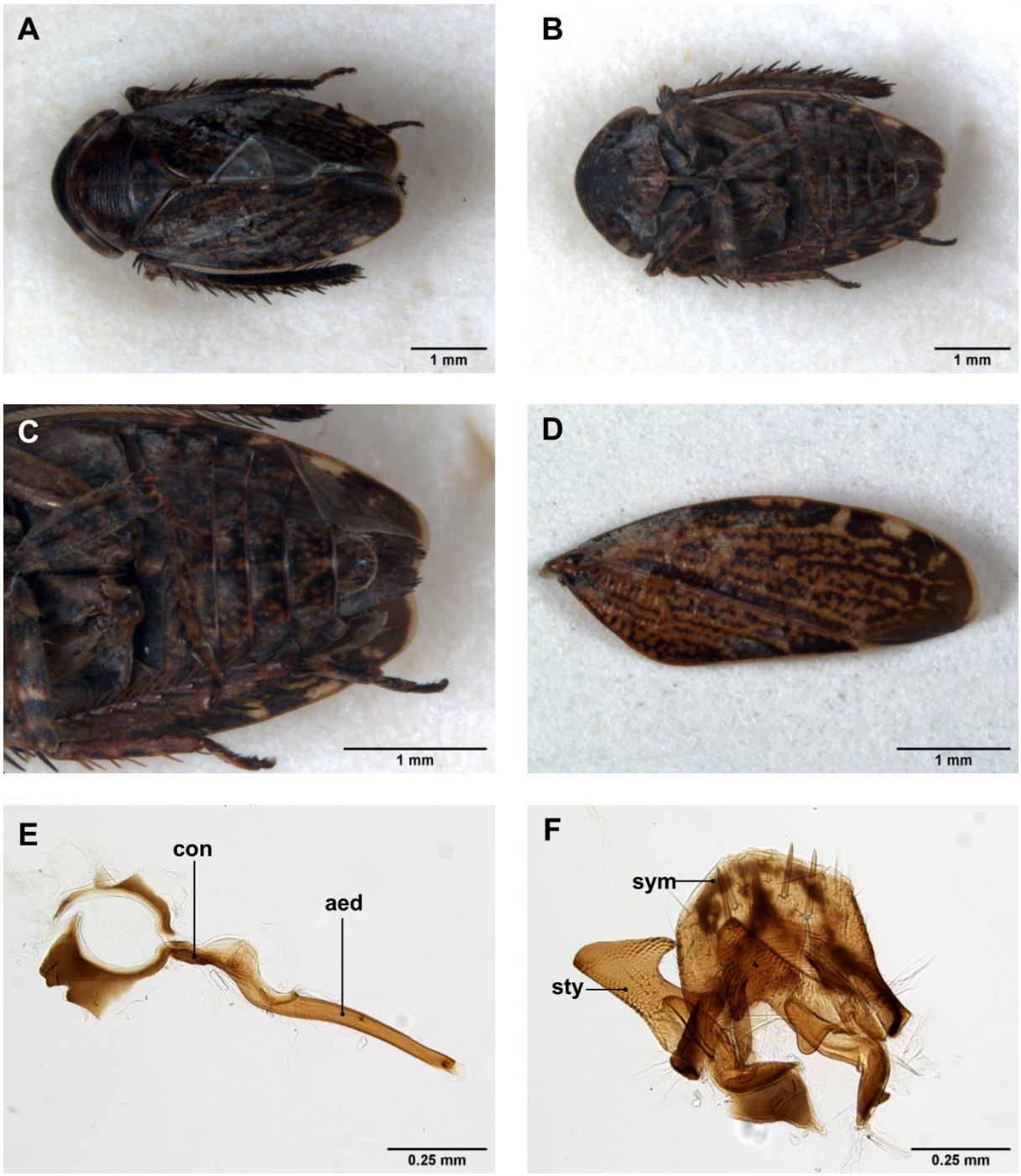

Figure D. 11 – Morphological aspects of *Goniagnathus brevis* (Herrich-Schäffer). **A** – Dorsal view. **B** – Ventral view. **C** – Detail of male genitalia in ventral view. **D** – Forewing. **E** – Aedeagus and connective. **F** – Male genital capsule. aed = aedeagus; allp = appendages of lateral lobe of pygofer; ast = anal style; atu = anal tube; con = connective; gep = genital plates; lowap = lower appendages of aedeagus; midap = middle appendages of aedeagus; pyg = pygofer; sty = styles; sym = sympodite; uppap = upper appendages of aedeagus.

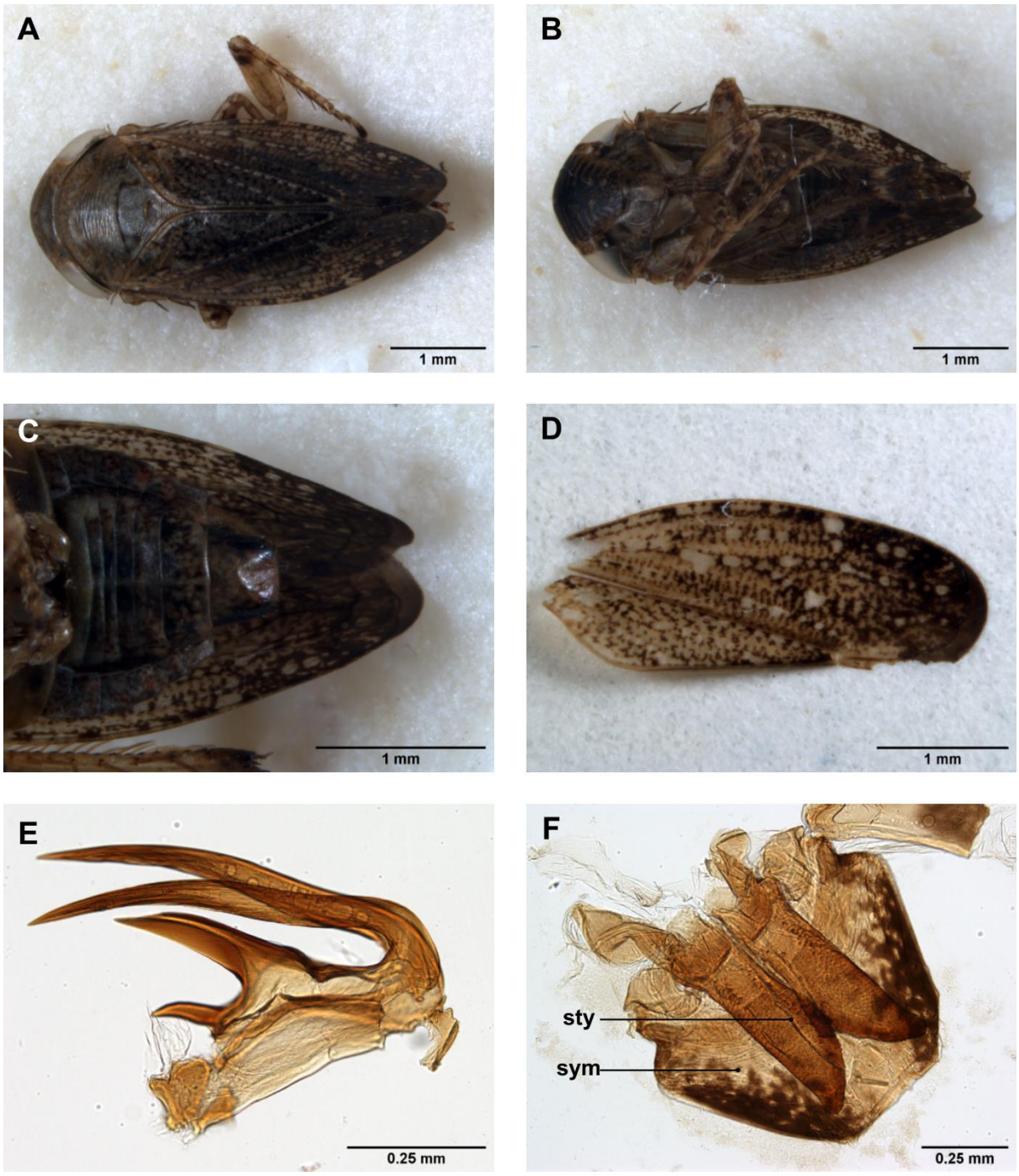

Figure D. 12 – Morphological aspects of *Goniagnathus guttulinervis* (Kirschbaum). **A** – Dorsal view. **B** – Ventral view. **C** – Detail of male genitalia in ventral view. **D** – Forewing. **E** – Aedeagus. **F** – Male genital capsule. aed = aedeagus; allp = appendages of lateral lobe of pygofer; ast = anal style; atu = anal tube; con = connective; gep = genital plates; lowap = lower appendages of aedeagus; midap = middle appendages of aedeagus; pyg = pygofer; sty = styles; sym = sympodite; uppap = upper appendages of aedeagus.

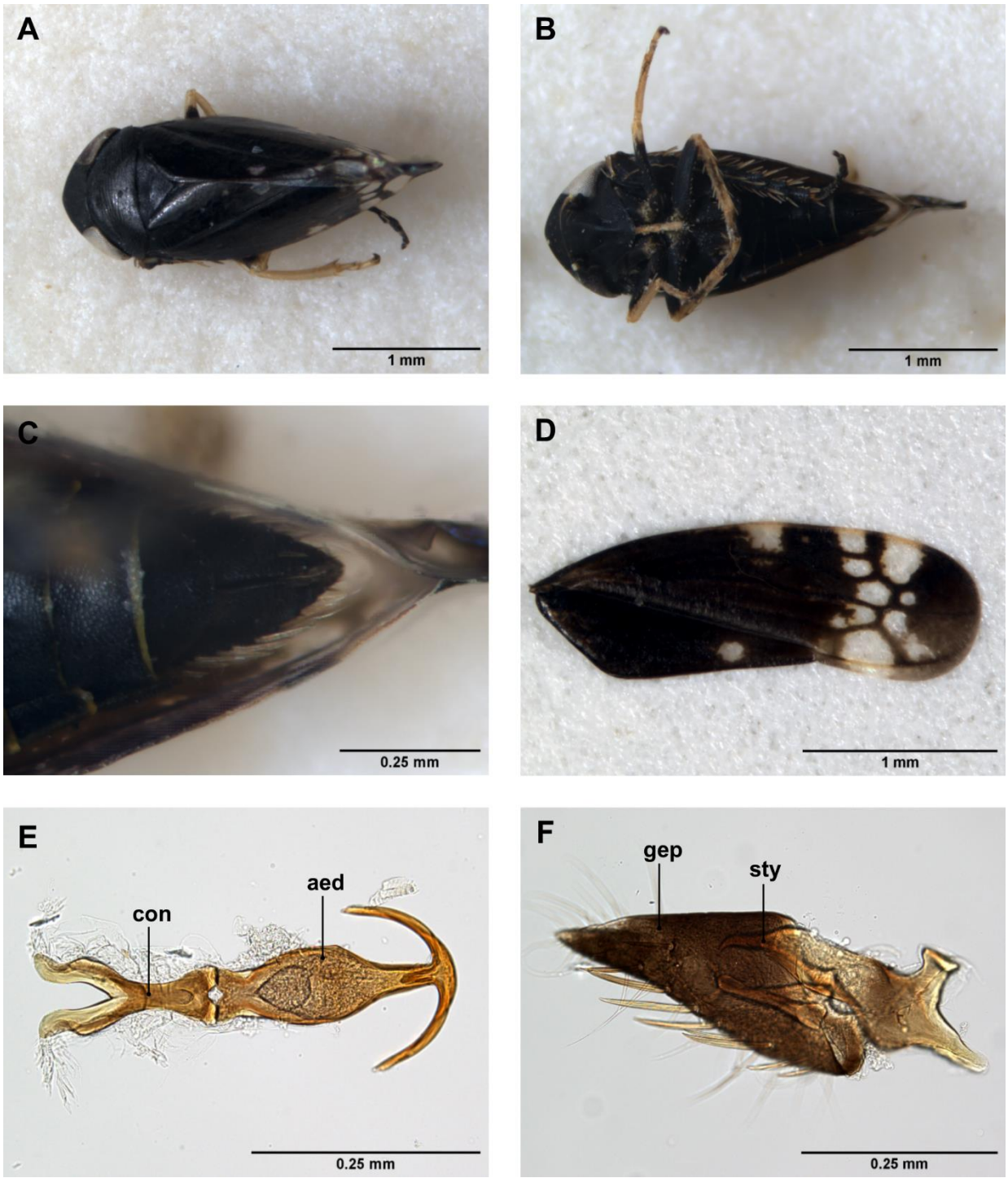

Figure D. 13 – Morphological aspects of *Neoaliturus fenestratus* (Herrich-Shäffer). **A** – Dorsal view. **B** – Ventral view. **C** – Detail of male genitalia in ventral view. **D** – Forewing. **E** – Aedeagus and connective. **F** – Genital plate and style. aed = aedeagus; allp = appendages of lateral lobe of pygofer; ast = anal style; atu = anal tube; con = connective; gep = genital plates; lowap = lower appendages of aedeagus; midap = middle appendages of aedeagus; pyg = pygofer; sty = styles; sym = sympodite; uppap = upper appendages of aedeagus.

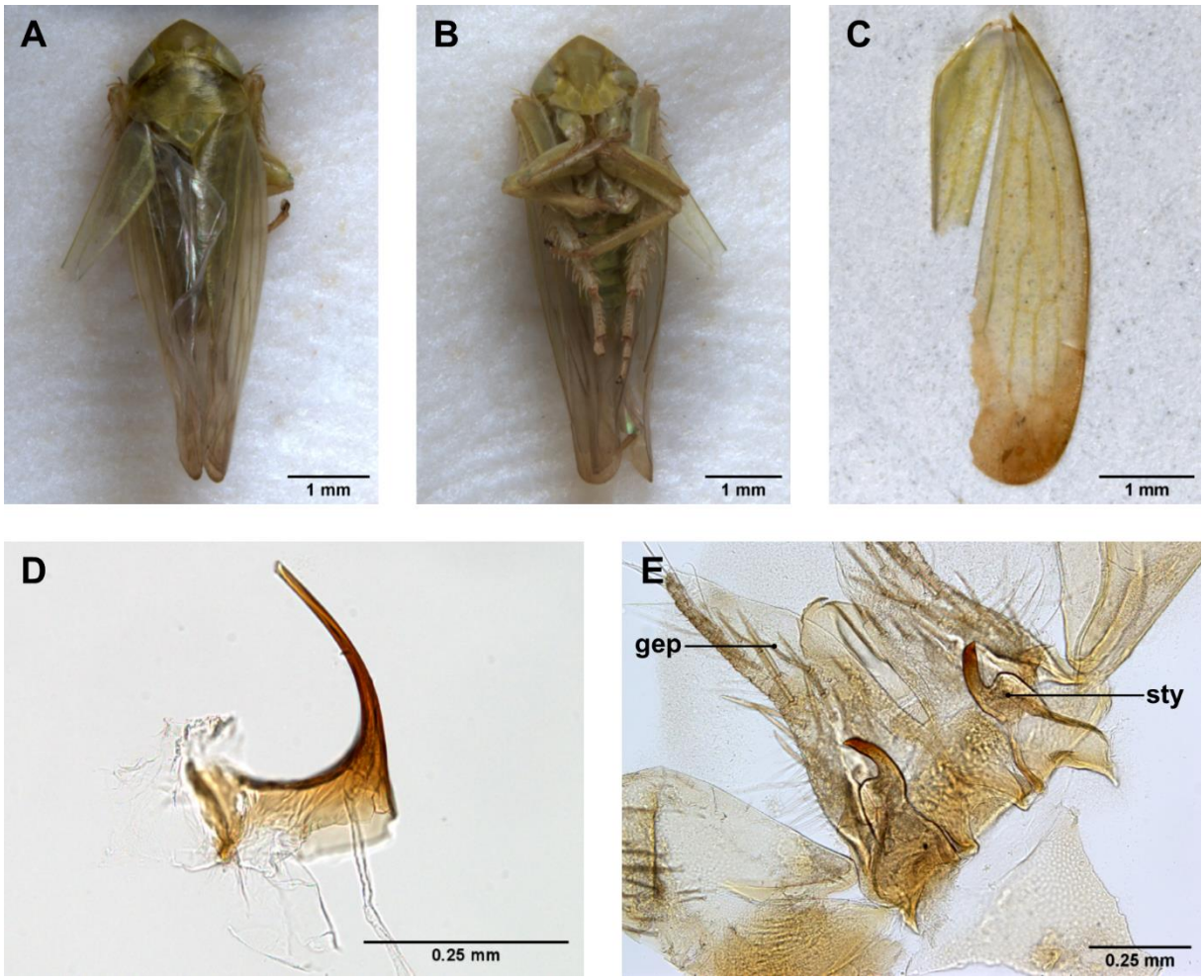

Figure D. 14 – Morphological aspects of *Oxytettigella viridinervis* (Kirschbaum). **A** – Dorsal view. **B** – Ventral view. **C** – Forewing**. D** – Aedeagus. **E** – Male genital capsule. aed = aedeagus; allp = appendages of lateral lobe of pygofer; ast = anal style; atu = anal tube; con = connective; gep = genital plates; lowap = lower appendages of aedeagus; midap = middle appendages of aedeagus; pyg = pygofer; sty = styles; sym = sympodite; uppap = upper appendages of aedeagus.

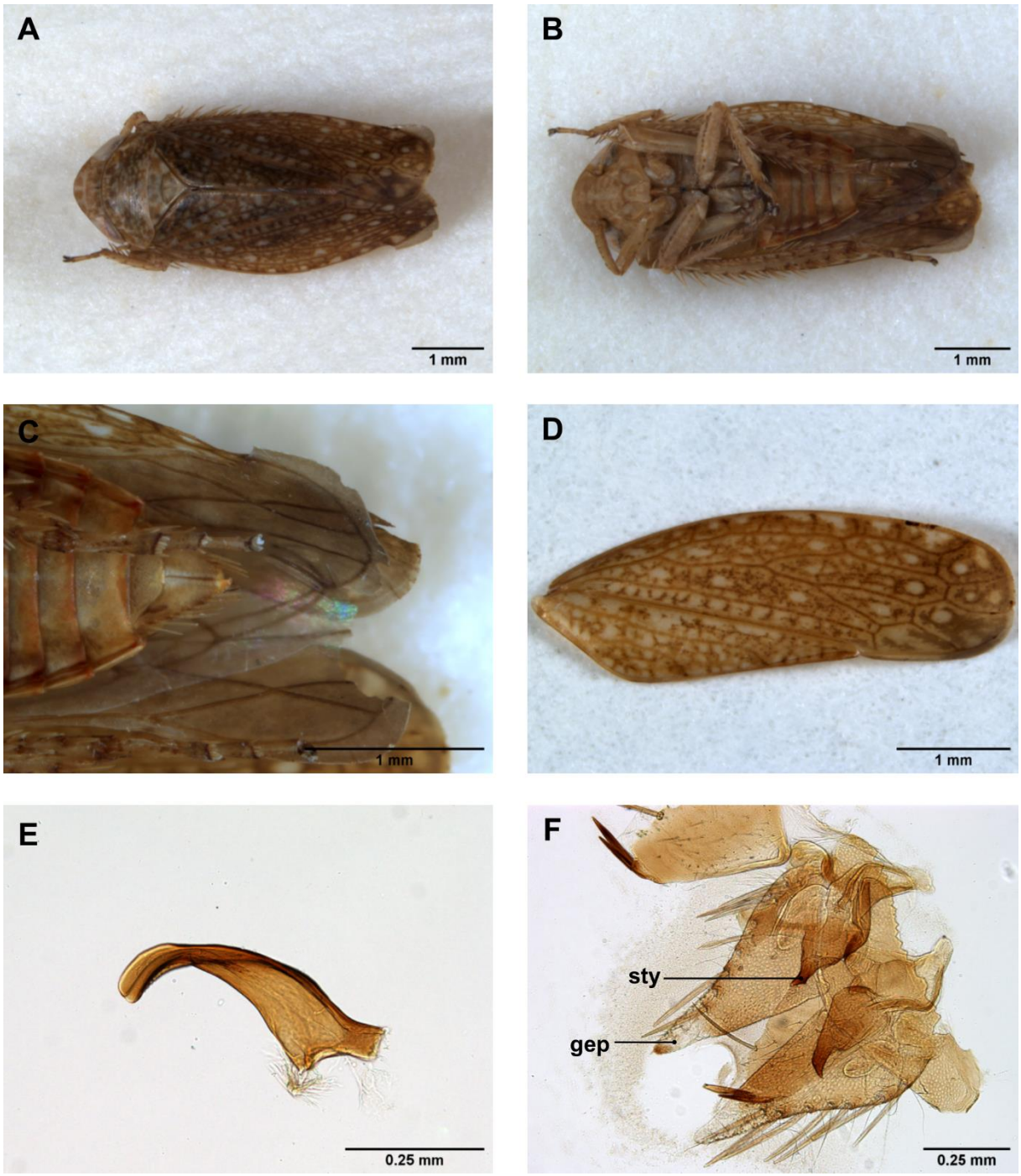

Figure D. 15 – Morphological aspects of *Phlepsius spinulosus* Wagner. **A** – Dorsal view. **B** – Ventral view. **C** – Detail of male genitalia in ventral view. **D** – Forewing. **E** – Aedeagus. **F** – Male genital capsule. aed = aedeagus; allp = appendages of lateral lobe of pygofer; ast = anal style; atu = anal tube; con = connective; gep = genital plates; lowap = lower appendages of aedeagus; midap = middle appendages of aedeagus; pyg = pygofer; sty = styles; sym = sympodite; uppap = upper appendages of aedeagus.

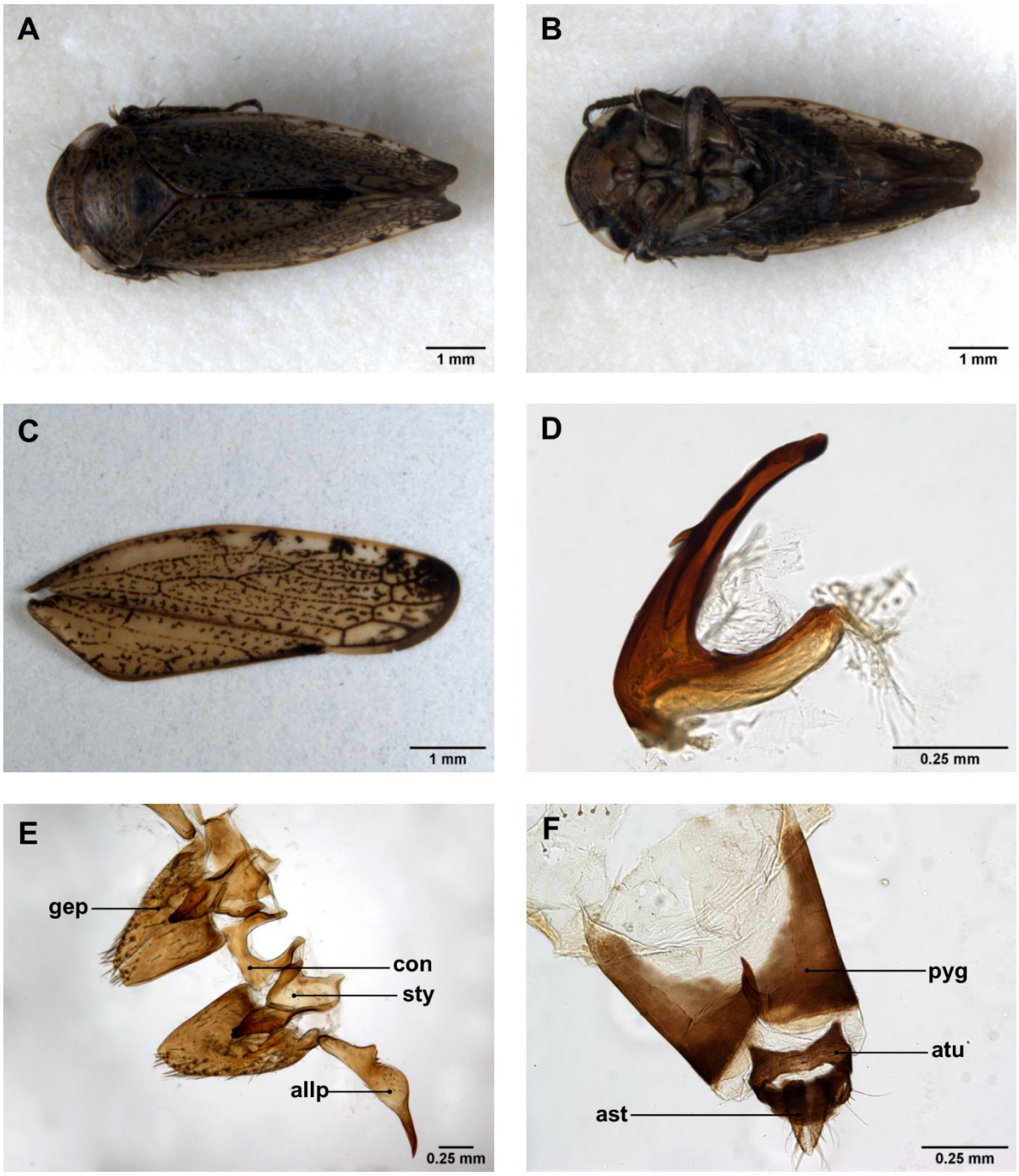

Figure D. 16 – Morphological aspects of *Selenocephalus conspersus* (Herrich-Schäffer). **A** – Dorsal view. **B** – Ventral view. **C** – Forewing. **D** – Aedeagus. **E, F** – Male genital capsule. aed = aedeagus; allp = appendages of lateral lobe of pygofer; ast = anal style; atu = anal tube; con = connective; gep = genital plates; lowap = lower appendages of aedeagus; midap = middle appendages of aedeagus; pyg = pygofer; sty = styles; sym = sympodite; uppap = upper appendages of aedeagus.

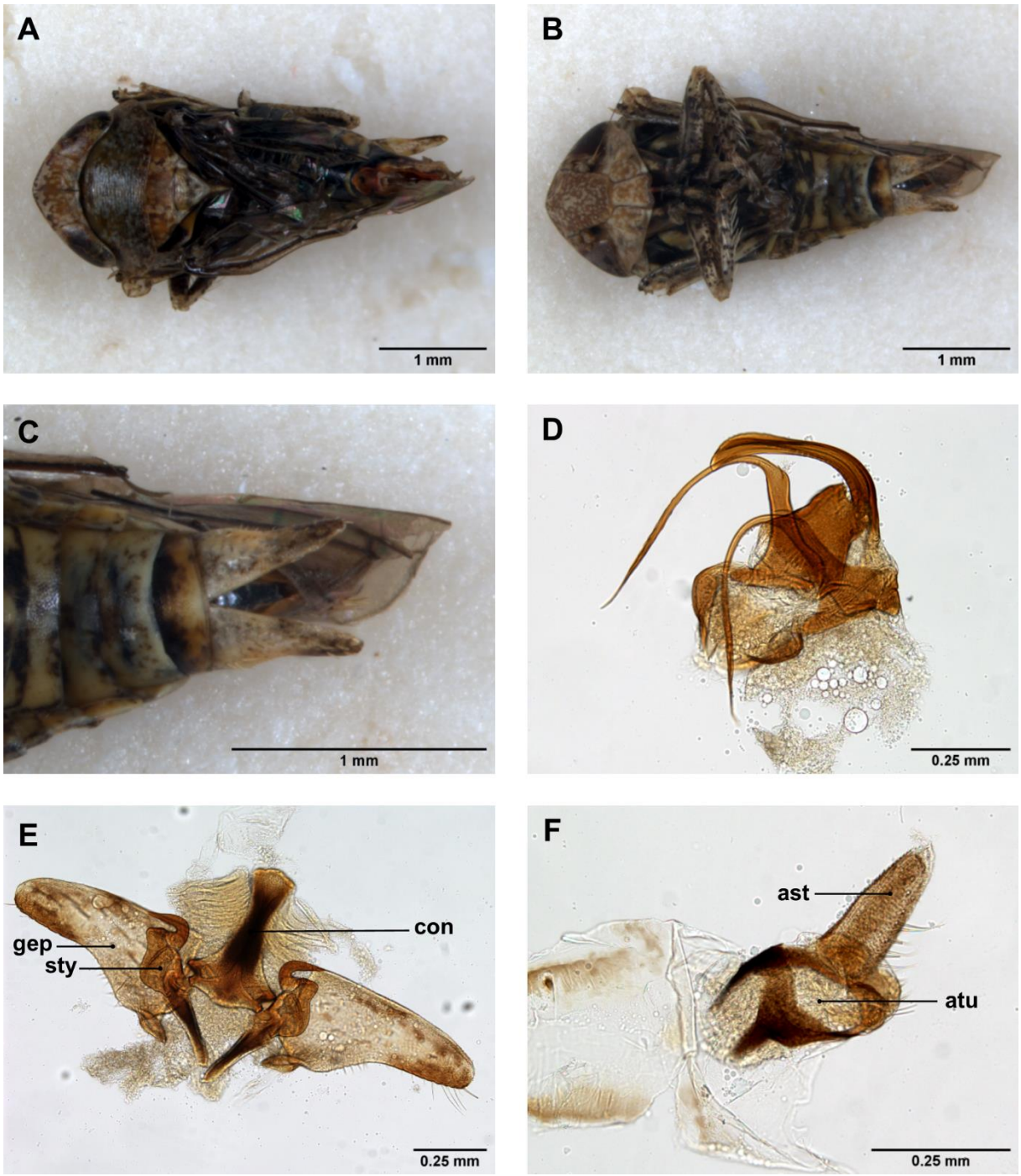

Figure D. 17 – Morphological aspects of *Stegelytra putoni* Mulsant & Rey. **A** – Dorsal view. **B** – Ventral view. **C** – Detail of male genitalia in ventral view. **D** – Aedeagus. **E, F** – Male genital capsule. aed = aedeagus; allp = appendages of lateral lobe of pygofer; ast = anal style; atu = anal tube; con = connective; gep = genital plates; lowap = lower appendages of aedeagus; midap = middle appendages of aedeagus; pyg = pygofer; sty = styles; sym = sympodite; uppap = upper appendages of aedeagus.

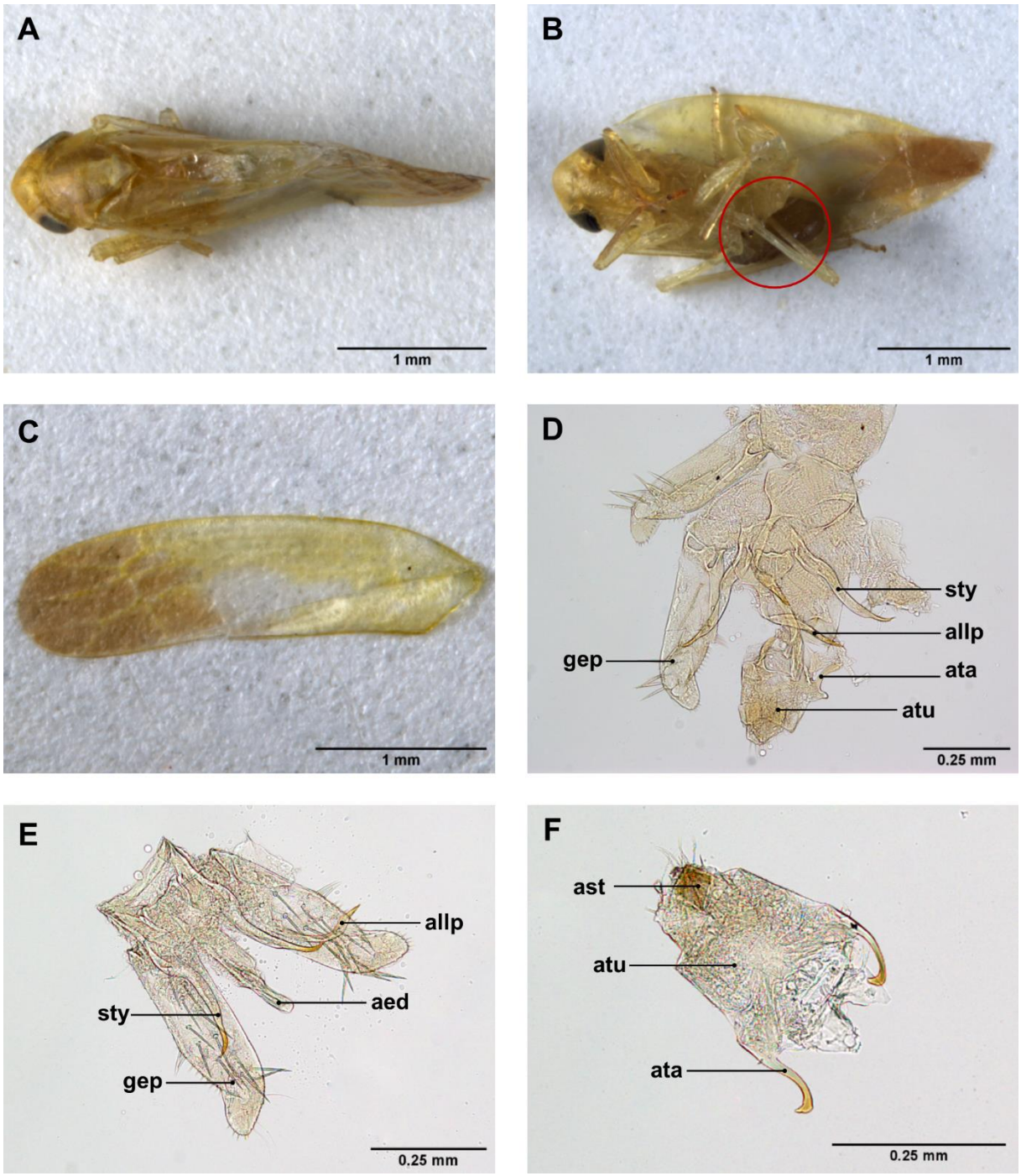

Figure D. 18 – Morphological aspects of Typhlocybinae. Parasitized *Empoasca solani* (Curtis): **A** – Dorsal view. **B** – Ventral view with parasitoid insertion. **C** – Forewing. **D** – Male genital capsule. *Empoasca decipiens* Paoli: **E, F** – Male genital capsule. aed = aedeagus; allp = appendages of lateral lobe of pygofer; ast = anal style; atu = anal tube; con = connective; gep = genital plates; lowap = lower appendages of aedeagus; midap = middle appendages of aedeagus; pyg = pygofer; sty = styles; sym = sympodite; uppap = upper appendages of aedeagus.

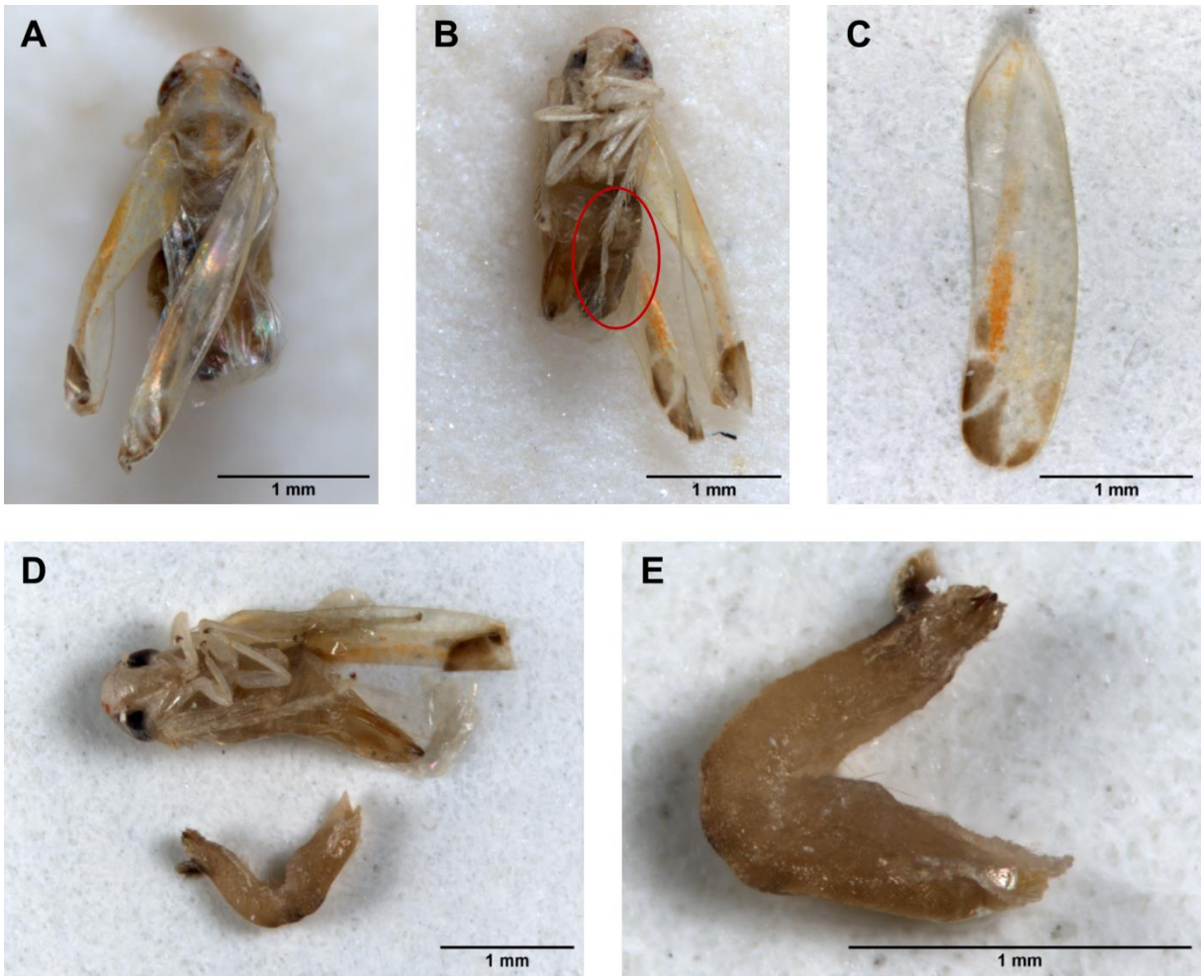

Figure D. 19 – Parasitized *Lindbergina aurovittata* (Douglas). **A** – General morphology (dorsal view). **B** – General morphology with parasitoid insertion (ventral view). **C** – Forewing. **D** – Side by side comparison between host and dryinid larva. **E** – Dryinid larva.

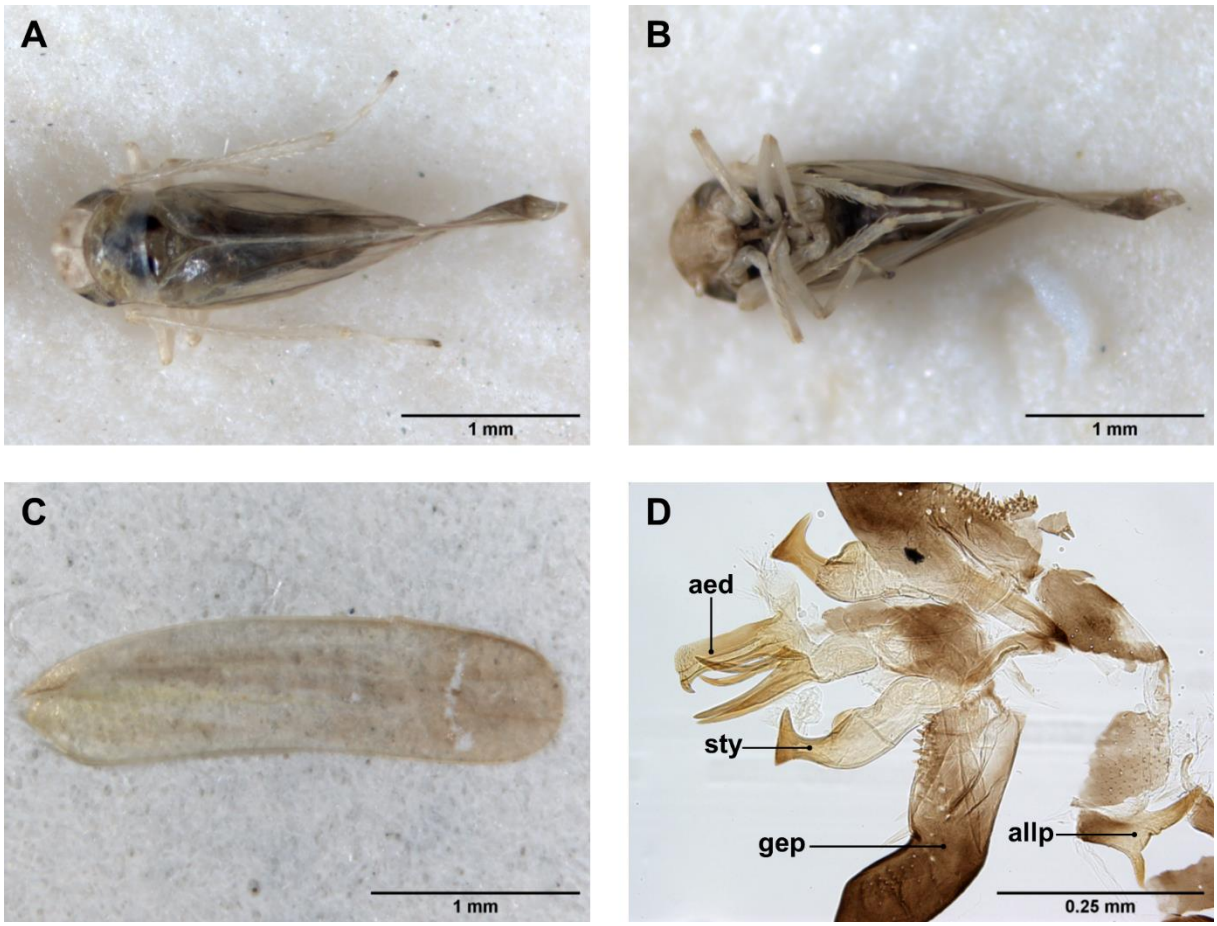

Figure D. 20 – Morphological aspects of *Zyginidia scutellaris* (Herrich-Schäffer). **A** – Dorsal view. **B** – Ventral view. **C** – Forewing. **D** – Male genital capsule. aed = aedeagus; allp = appendages of lateral lobe of pygofer; ast = anal style; atu = anal tube; con = connective; gep = genital plates; lowap = lower appendages of aedeagus; midap = middle appendages of aedeagus; pyg = pygofer; sty = styles; sym = sympodite; uppap = upper appendages of aedeagus.

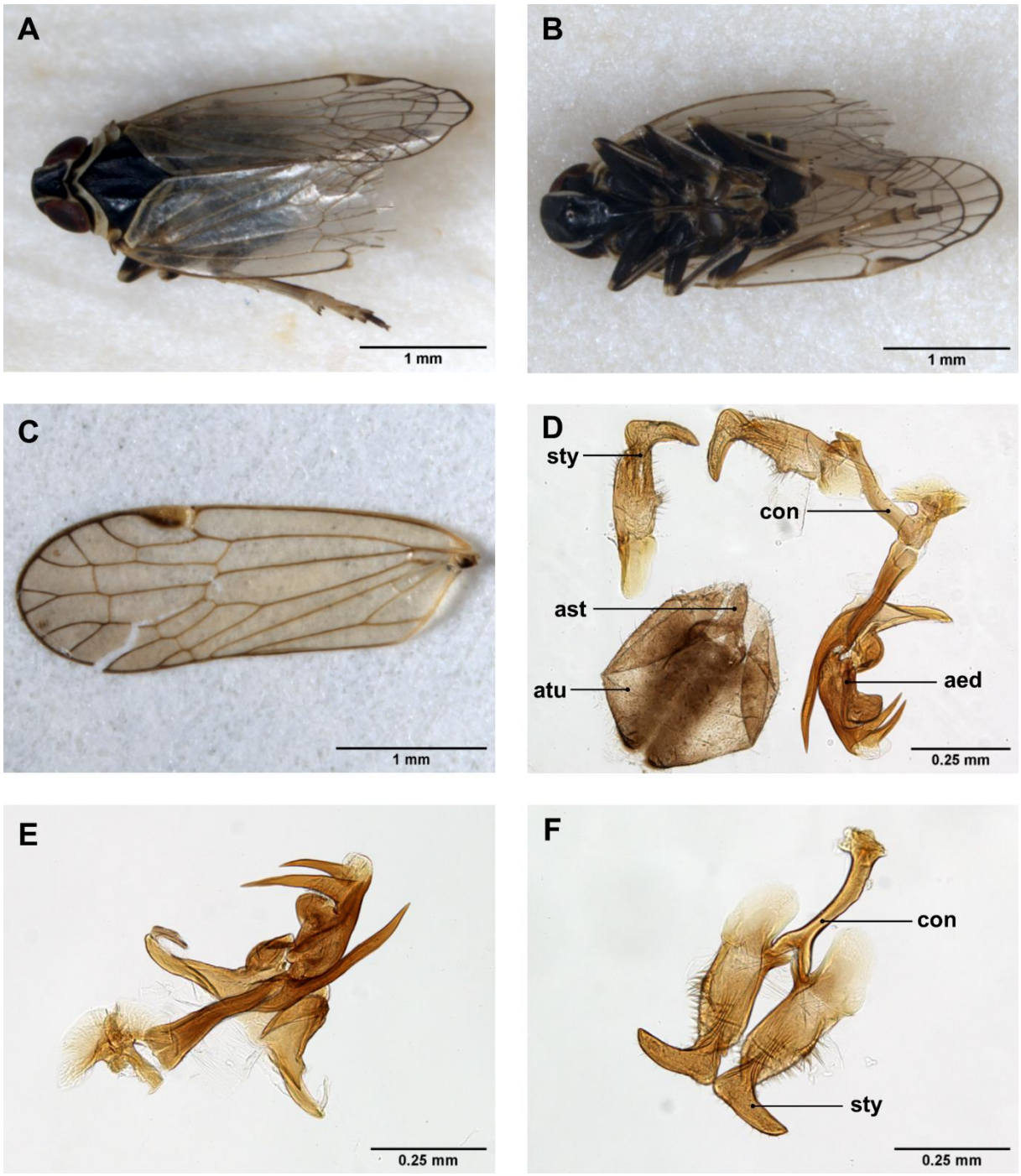

Figure D. 21 – Morphological aspects of Cixiinae. *Hyalesthes obsoletus* Signoret: **A** – Dorsal view. **B** – Ventral view. **C** – Forewing. **D** – Male genital capsule. *Hyalesthes luteipes* Fieber: **E** – Aedeagus. **F** – Styles and connective. aed = aedeagus; allp = appendages of lateral lobe of pygofer; ast = anal style; atu = anal tube; con = connective; gep = genital plates; lowap = lower appendages of aedeagus; midap = middle appendages of aedeagus; pyg = pygofer; sty = styles; sym = sympodite; uppap = upper appendages of aedeagus.

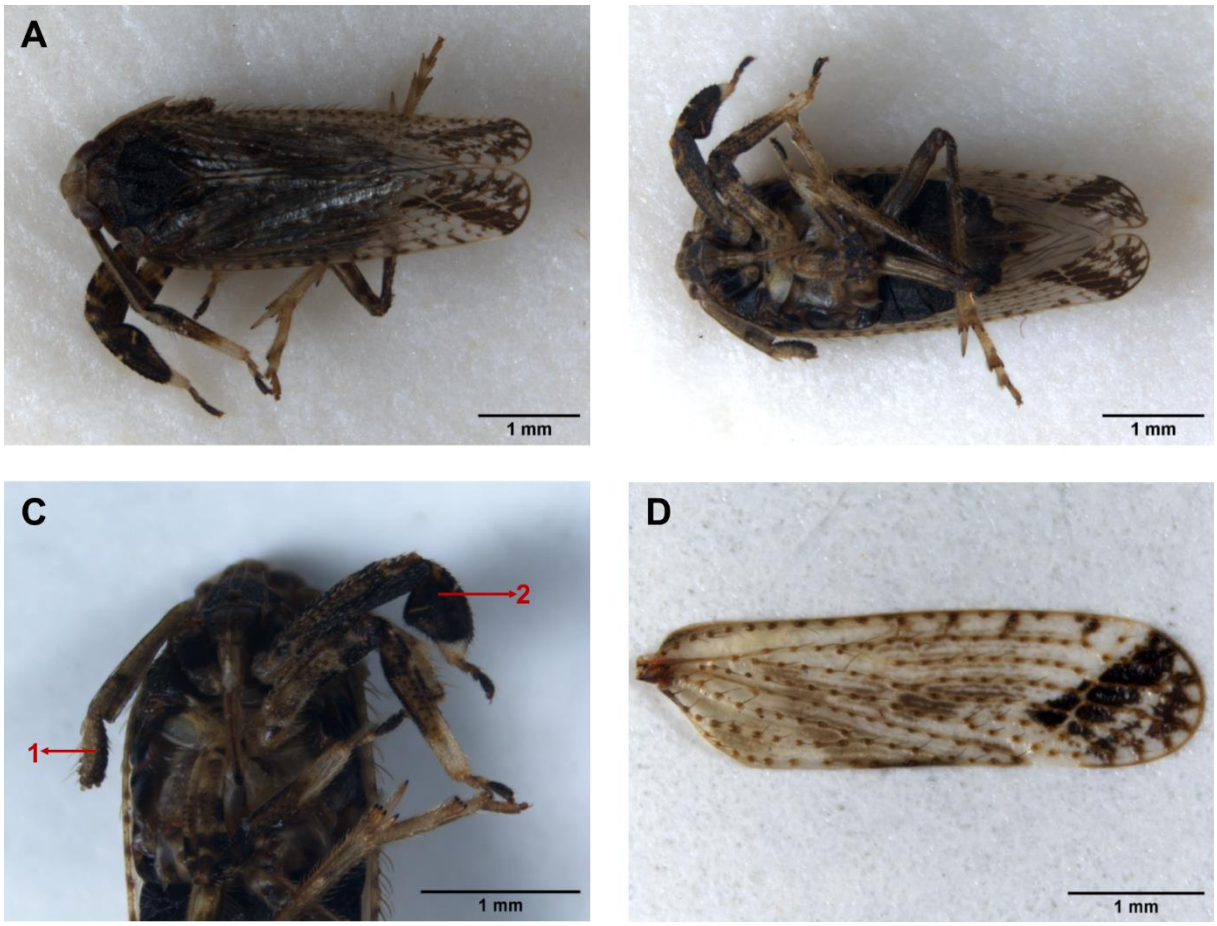

Figure D. 22 – Morphological aspects of *Asiraca clavicornis* (Fabricius). **A** – Dorsal view. **B** – Ventral view. **C** – Details of 1 - first antennal segment, 2 – frontal legs. **D** – Forewing.

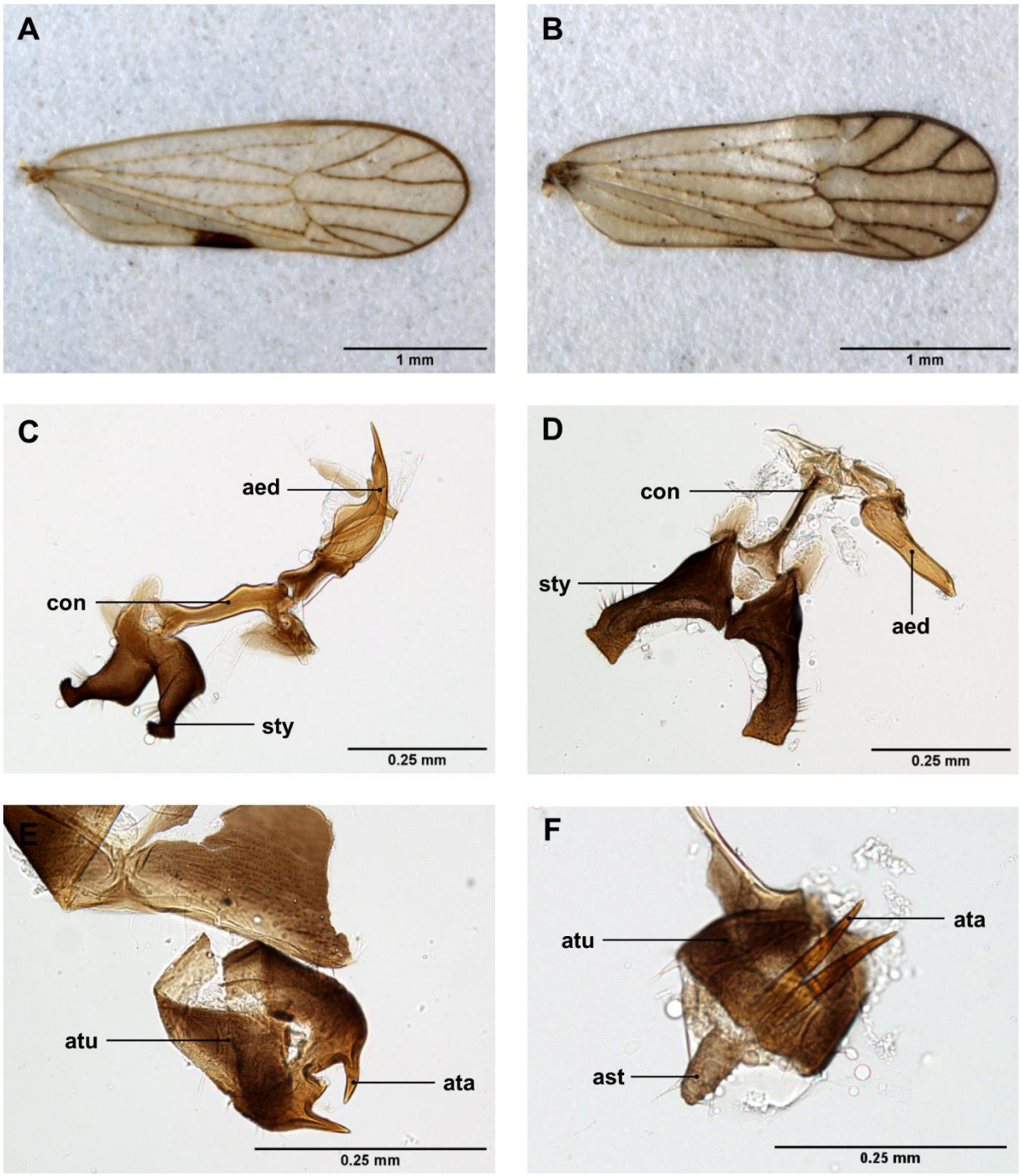

Figure D. 23 – Morphological aspects of Delphacinae. *Laodelphax striatella* (Fallén): **A** – Forewing. **C** – Aedeagus and connective. **E** – Anal tube and anal tube appendages. *Metadelphax propinqua* (Fieber): **B** – Forewing. **D, F** – Male genital capsule. aed = aedeagus; allp = appendages of lateral lobe of pygofer; ast = anal style; atu = anal tube; con = connective; gep = genital plates; lowap = lower appendages of aedeagus; midap = middle appendages of aedeagus; pyg = pygofer; sty = styles; sym = sympodite; uppap = upper appendages of aedeagus.

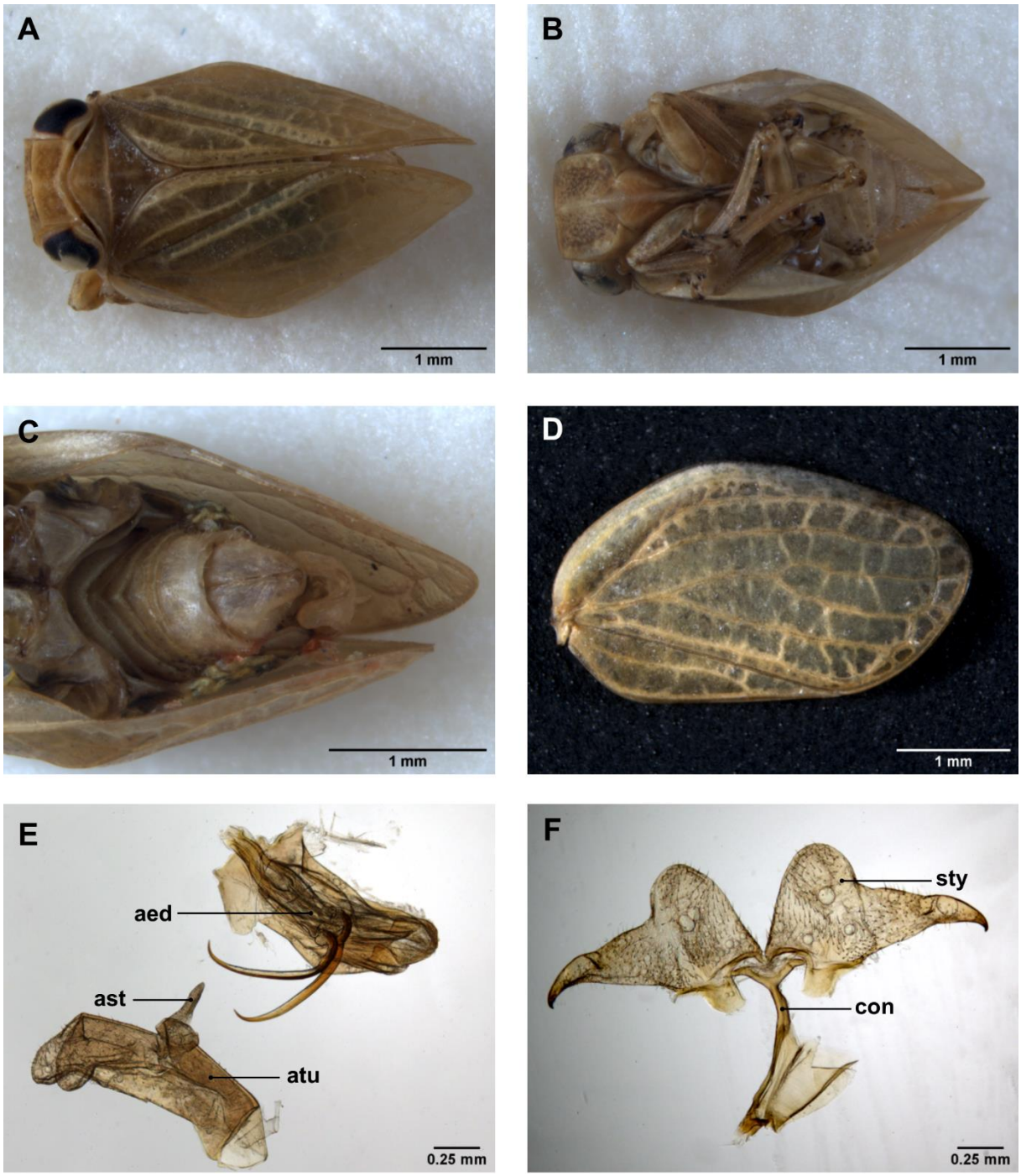

Figure D. 24 – Morphological aspects of *Agalmatium bilobum* (Fieber). **A** – Dorsal view. **B** – Ventral view. **C** – Detail of male genitalia in ventral view. **D** – Forewing. **E** – Aedeagus, anal tube and anal style. **F** – Styles and connective. aed = aedeagus; allp = appendages of lateral lobe of pygofer; ast = anal style; atu = anal tube; con = connective; gep = genital plates; lowap = lower appendages of aedeagus; midap = middle appendages of aedeagus; pyg = pygofer; sty = styles; sym = sympodite; uppap = upper appendages of aedeagus.

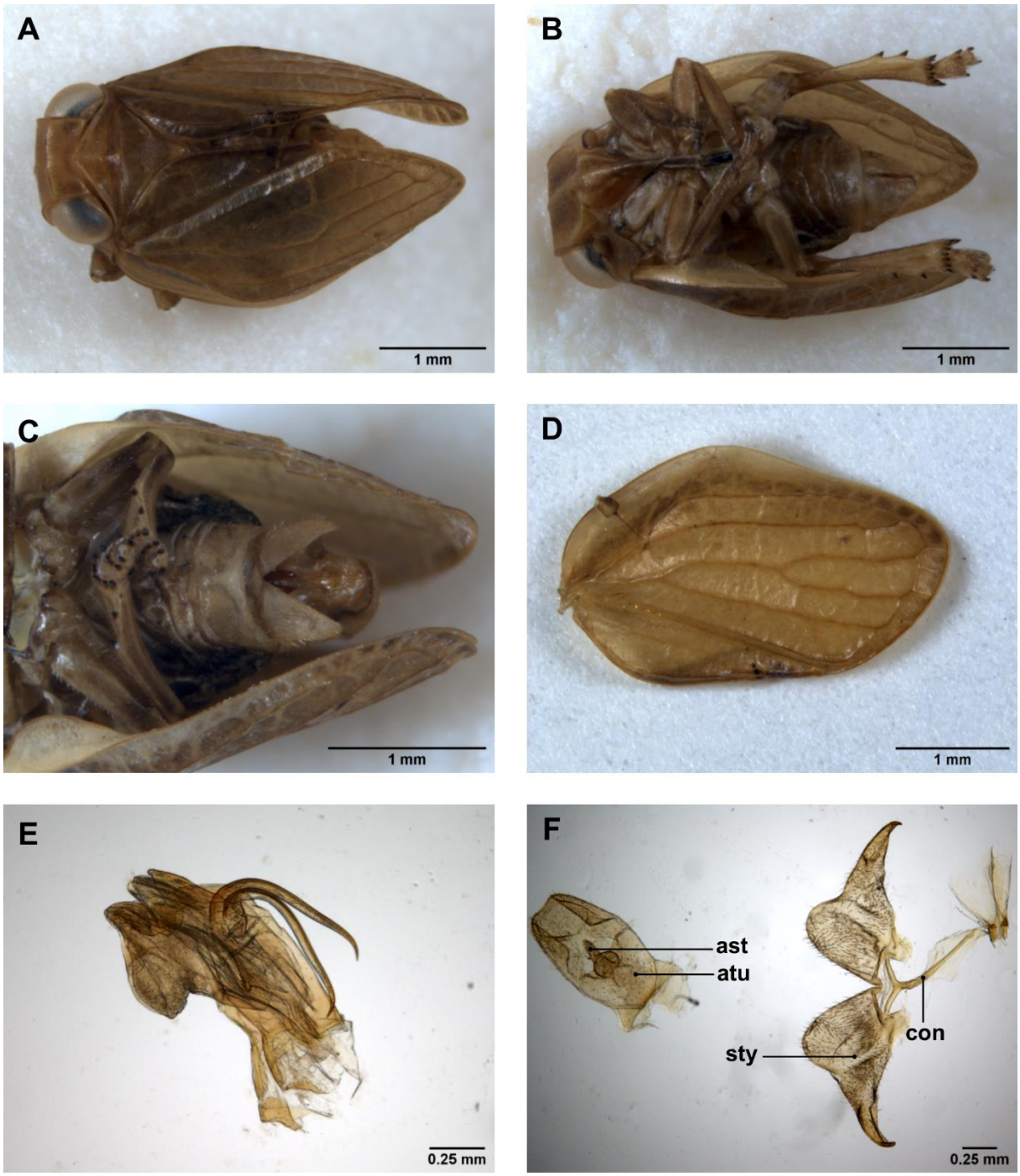

Figure D. 25 – Morphological aspects of *Agalmatium flavescens* (Olivier). **A** – Dorsal view. **B** – Ventral view. **C** – Detail of male genitalia in ventral view. **D** – Forewing. **E** – Aedeagus **F** – Male genital capsule. aed = aedeagus; allp = appendages of lateral lobe of pygofer; ast = anal style; atu = anal tube; con = connective; gep = genital plates; lowap = lower appendages of aedeagus; midap = middle appendages of aedeagus; pyg = pygofer; sty = styles; sym = sympodite; uppap = upper appendages of aedeagus.

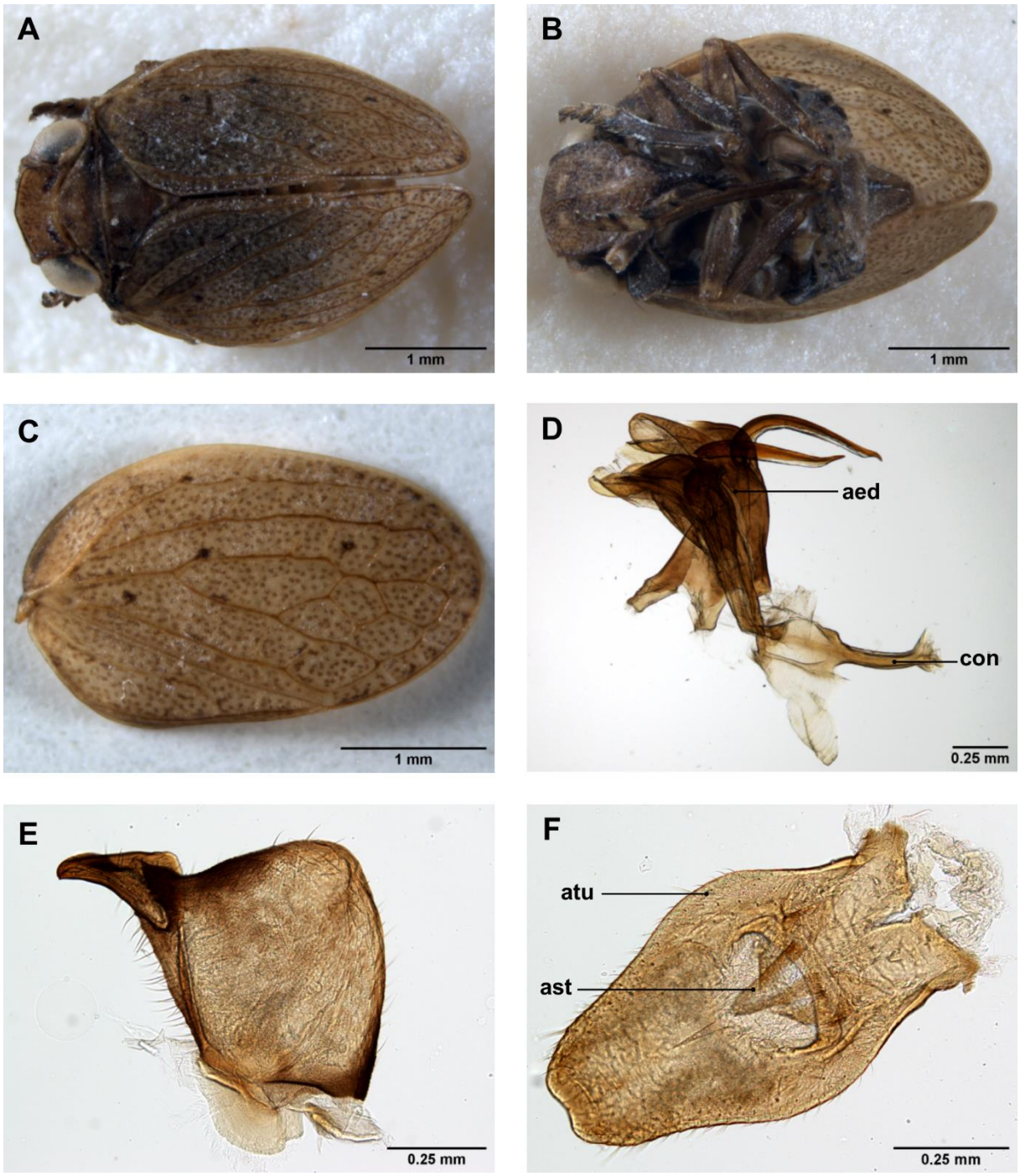

Figure D. 26 – Morphological aspects of *Palmallorcus punctulatus* (Rambur). **A** – Dorsal view. **B** – Ventral view. **C** – Forewing. **D** – Aedeagus and connective. **E** – Style. **F** – Anal tube with anal style. aed = aedeagus; allp = appendages of lateral lobe of pygofer; ast = anal style; atu = anal tube; con = connective; gep = genital plates; lowap = lower appendages of aedeagus; midap = middle appendages of aedeagus; pyg = pygofer; sty = styles; sym = sympodite; uppap = upper appendages of aedeagus.

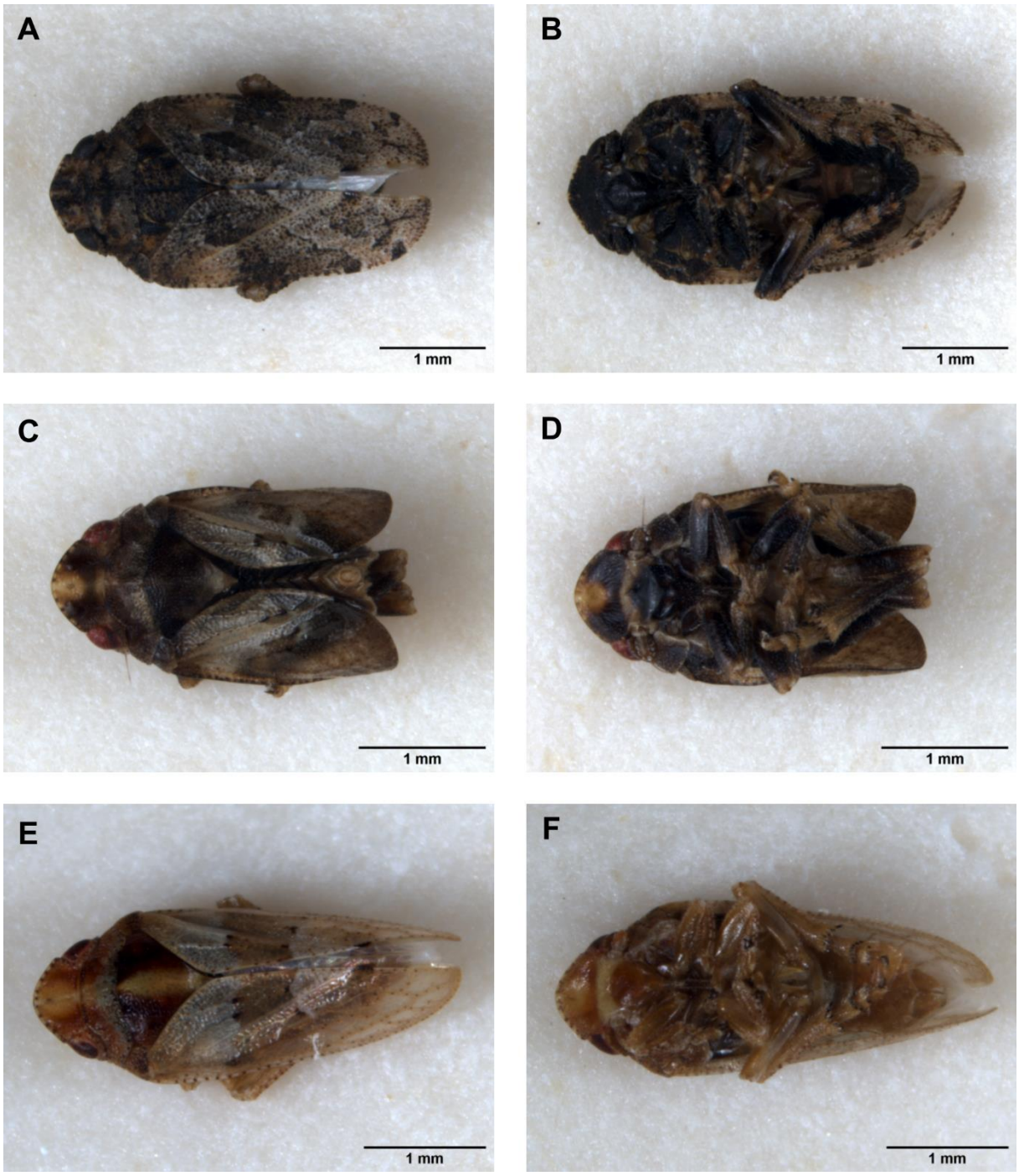

Figure D. 27 – Morphological aspects of Tettigometrinae. *Tettigometra costulata* Fieber: **A** – Dorsal view. **B** – Ventral view. *Tettigometra impressifrons* Mulsant & Rey: **C** – Dorsal view. **D** – Ventral view. *Tettigometra obliqua* Panzer: **E** – Dorsal view. **F** – Ventral view.

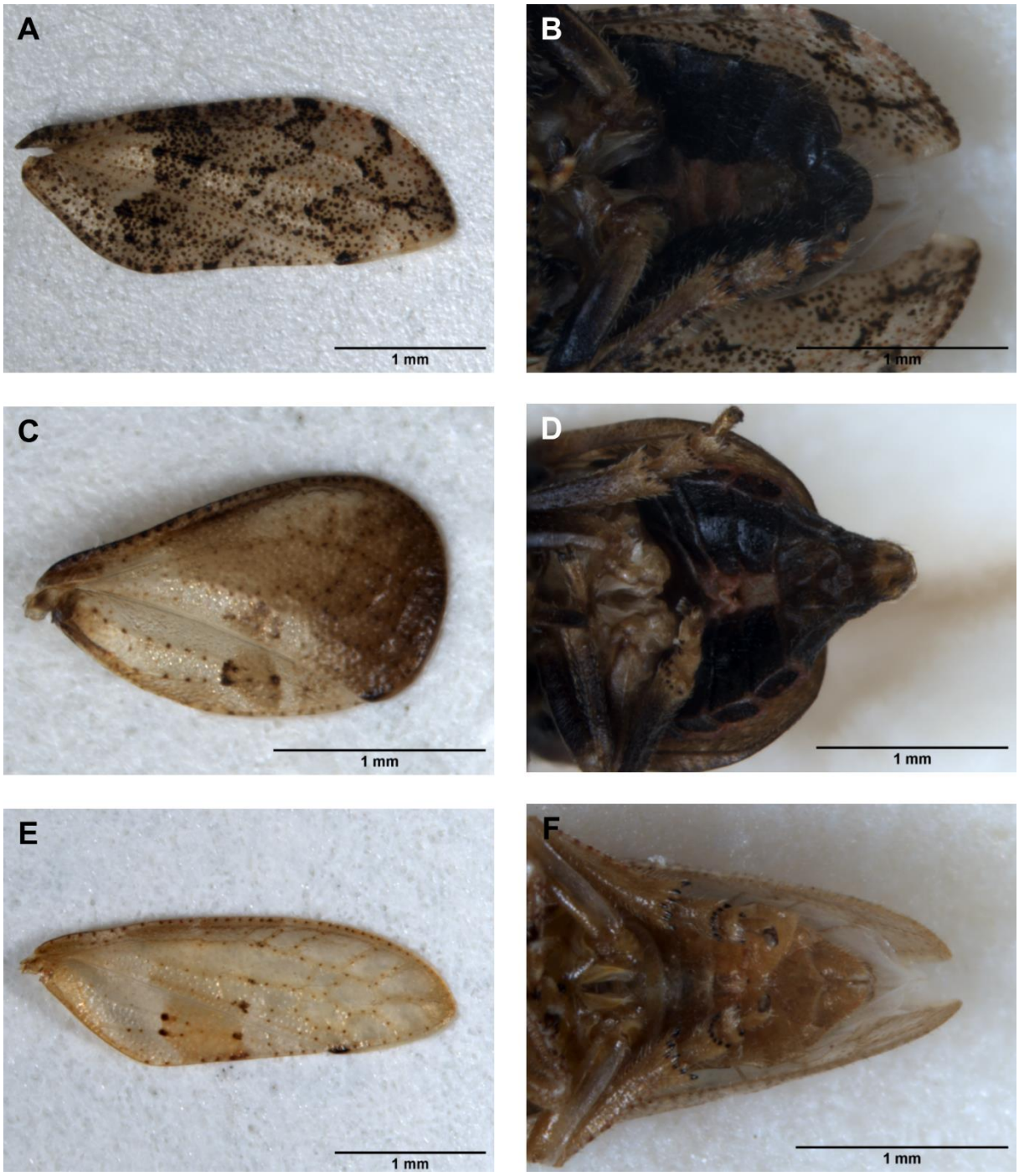

Figure D. 28 – Morphological aspects of Tettigometrinae. *Tettigometra costulata* Fieber: **A** – Forewing. **B** – Detail of male genitalia in ventral view. *Tettigometra impressifrons* Mulsant & Rey: **C** – Forewing. **D** – Detail of male genitalia in ventral view. *Tettigometra obliqua* Panzer: **E** – Forewing. **F** – Detail of male genitalia in ventral view.

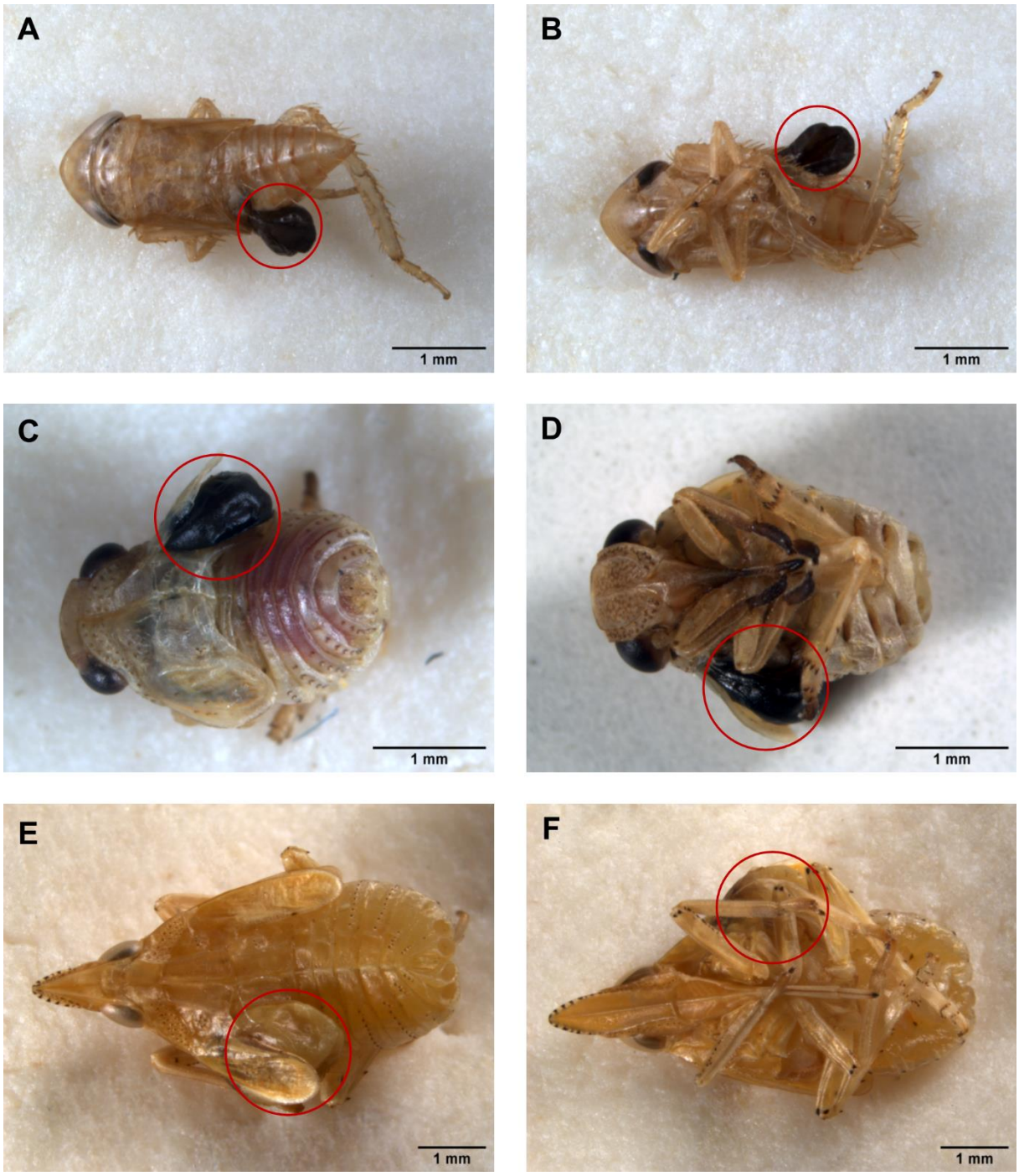

Figure D. 29 – Parasitized nymphs. Cicadomorpha general morphology: **A** – Dorsal view with parasitoid insertion. **B** – Ventral view with parasitoid insertion. Fulgoromorpha general morphology: **C, E** – dorsal view with parasitoid insertion. **D, F** – ventral view with parasitoid insertion.

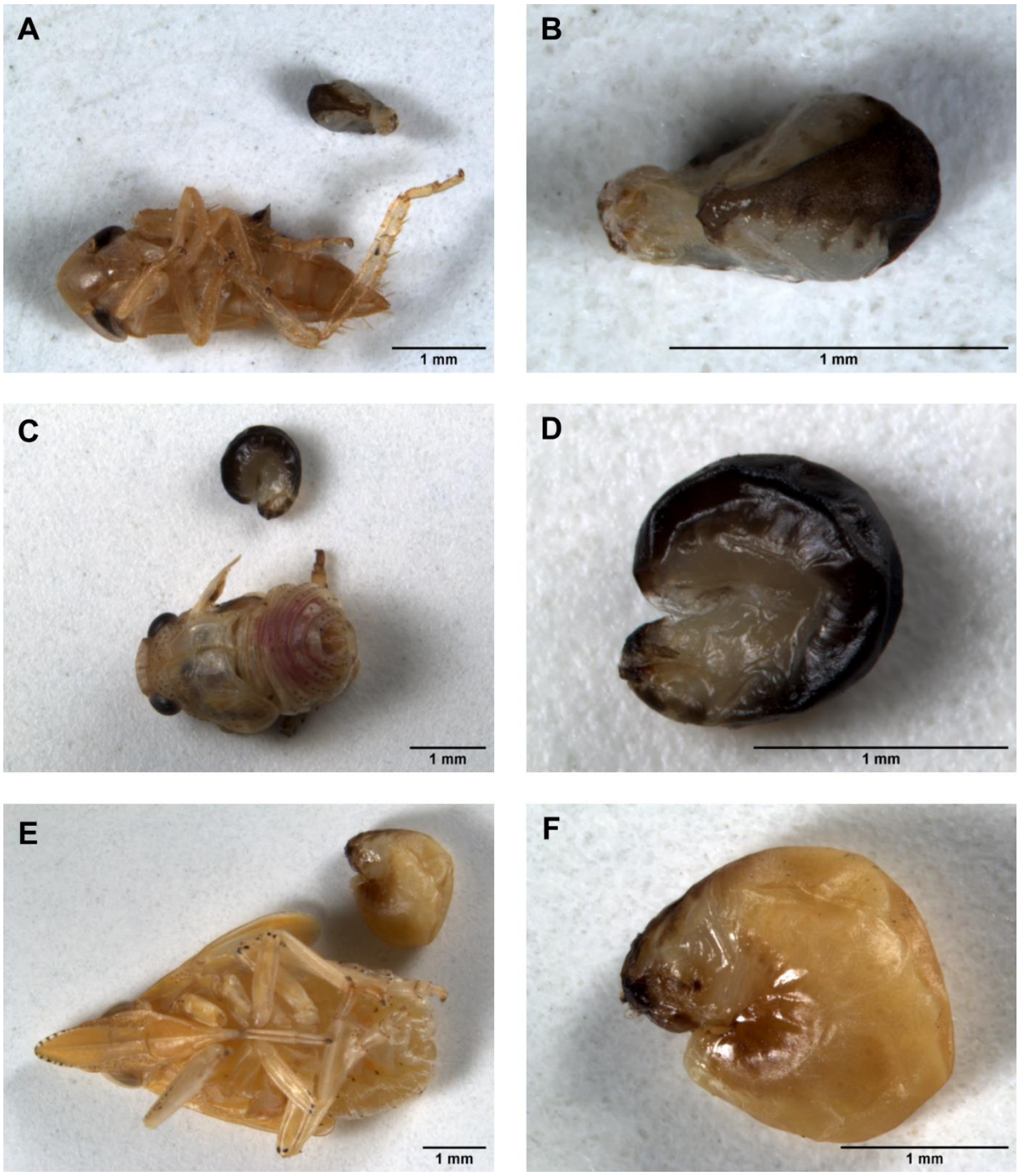

Figure D. 30 – Parasitized nymphs. Cicadomorpha: **A** – Side by side comparison between host and dryinid larva. Fulgoromorpha: **C, E** – Side by side comparison between host and dryinid larva. **B, D, F** – Dryinid larva.

Annex E – Pool composition

Table E. 1 - Information about each pool used for detection of *Xylella fastidiosa* with qPCR tests. Coordinates of the sampling points are presented in decimal degrees. N = number of individuals; GU = geographic unit; F = female; M = male.

Pool	N	Species	Sex	GU	Plant host	Latitude	Longitude
1	1	*Lepyronia coleoptrata*	F	21	*Convolvulus arvensis*	38.094680	-7.254195
1	1	*Lepyronia coleoptrata*	M	21	*Convolvulus arvensis*	38.094680	-7.254195
2	1	*Neophilaenus campestris*	F	0	*Olea europaea*	38.988917	-8.291456
3	1	*Neophilaenus campestris*	F	8	*Olea europaea*	38.755243	-7.729206
4	1	*Neophilaenus campestris*	M	20	*Convolvulus arvensis*	38.198422	-7.856793
5	1	*Neophilaenus campestris*	M	25	*Olea europaea*	37.882200	-8.158100
6	1	*Neophilaenus campestris*	M	26	*Olea europaea*	37.961375	-7.618799
7	1	*Philaenus spumarius*	M	0	*Daucus carota*	38.937164	-8.485281
7	1	*Philaenus* sp.	F	0	*Galactites tomentosus*	38.937164	-8.485281
8	1	*Philaenus tesselatus*	F	2	*Olea europaea*	38.976093	-7.677234
9	1	*Philaenus tesselatus*	M	6	*Crepis capillaris*	38.685077	-8.485673
9	2	*Philaenus tesselatus*	M	6	*Chamaemelum mixtum*	38.685077	-8.485673
9	1	*Philaenus* sp.	F	6	*Olea europaea*	38.685077	-8.485673
10	1	*Philaenus* sp.	F	6	*Galactites tomentosus*	38.719690	-8.430842
10	1	*Philaenus* sp.	F	6	*Andryala integrifolia*	38.719690	-8.430842
11	1	*Philaenus* sp.	F	6	*Olea europaea*	38.773588	-8.368520
12	1	*Philaenus tesselatus*	M	7	*Convolvulus arvensis*	38.795766	-7.938138
13	1	*Philaenus* sp.	F	7	*Daucus carota*	38.655259	-8.205242
14	1	*Philaenus tesselatus*	F	8	*Olea europaea*	38.697196	-7.779009
14	1	*Philaenus tesselatus*	M	8	*Olea europaea*	38.697196	-7.779009
15	1	*Philaenus tesselatus*	F	8	*Olea europaea*	38.755243	-7.729206
15	2	*Philaenus tesselatus*	F	8	Mix ground cover	38.755243	-7.729206
16	1	*Philaenus tesselatus*	F	8	*Olea europaea*	38.766056	-7.713499
17	1	*Philaenus tesselatus*	M	8	*Olea europaea*	38.772255	-7.717580
18	1	*Philaenus tesselatus*	F	8	*Olea europaea*	38.833802	-7.641509
18	2	*Philaenus tesselatus*	M	8	*Olea europaea*	38.833802	-7.641509
19	1	*Philaenus tesselatus*	M	8	*Olea europaea*	38.819867	-7.825941
20	1	*Philaenus* sp.	F	9	*Foeniculum vulgare*	38.667503	-7.328936
20	2	*Philaenus* sp.	F	9	*Echium plantagineum*	38.667503	-7.328936
21	1	*Philaenus tesselatus*	F	9	*Olea europaea*	38.736348	-7.269122
22	1	*Philaenus tesselatus*	F	13	*Olea europaea*	38.525269	-8.240823
23	2	*Philaenus tesselatus*	F	14	*Olea europaea*	38.507804	-7.566162
24	2	*Philaenus tesselatus*	F	14	*Olea europaea*	38.486967	-7.736500
25	1	*Philaenus tesselatus*	F	15	*Olea europaea*	38.382020	-7.331507
26	2	*Philaenus tesselatus*	M	15	*Chamaemelum mixtum*	38.448920	-7.398881
26	2	*Philaenus tesselatus*	M	15	*Elaeoselinum foetidum*	38.448920	-7.398881
27	1	*Philaenus* sp.	F	15	*Scabiosa atropurpurea*	38.544176	-7.483825
27	1	*Philaenus* sp.	F	15	*Daucus carota*	38.544176	-7.483825
27	1	*Philaenus* sp.	F	15	*Andryala integrifolia*	38.544176	-7.483825
28	2	*Philaenus tesselatus*	F	19	*Olea europaea*	38.24448	-7.945658
29	1	*Philaenus tesselatus*	M	19	*Echium plantagineum*	38.166765	-8.143498
29	1	*Philaenus tesselatus*	M	19	*Conium maculatum*	38.166765	-8.143498
30	1	*Philaenus tesselatus*	F	20	*Olea europaea*	38.121436	-7.837334
31	1	*Philaenus tesselatus*	M	20	*Andryala integrifolia*	38.317153	-7.698278
32	1	*Philaenus tesselatus*	F	21	*Lavatera trimestris*	38.094680	-7.254195
33	1	*Philaenus tesselatus*	F	21	*Ridolfia segetum*	38.131275	-7.329533
33	1	*Philaenus tesselatus*	M	21	*Ridolfia segetum*	38.131275	-7.329533
34	1	*Philaenus tesselatus*	F	21	*Olea europaea*	38.156567	-7.425753
35	1	*Philaenus tesselatus*	M	21	*Olea europaea*	38.218225	-7.542429
36	1	*Philaenus tesselatus*	M	26	*Olea europaea*	37.961375	-7.618799
37	1	*Philaenus tesselatus*	F	27	*Torilis* sp.	37.944818	-7.316707
37	1	*Philaenus tesselatus*	F	27	*Scabiosa atropurpurea*	37.944818	-7.316707
38	3	*Philaenus tesselatus*	M	27	Mix ground cover	38.026120	-7.300498

Table E.1 (cont.) – Information about each pool used for detection of *Xylella fastidiosa* with qPCR tests. Coordinates of the sampling points are presented in decimal degrees. N = number of individuals; GU = geographic unit; F = female; M = male.

Pool	N	Species	Sex	GU	Plant host	Latitude	Longitude
38	2	*Philaenus tesselatus*	F	27	Mix ground cover	38.026120	-7.300498
39	1	*Cercopis intermedia*	F	26	*Olea europaea*	37.960639	-7.806797
40	1	*Lepyronia coleoptrata*	M	3	*Verbascum sinuatum*	38.964189	-7.294191
40	1	*Lepyronia coleoptrata*	F	3	*Verbascum sinuatum*	38.964189	-7.294191
41	1	*Philaenus tesselatus*	M	3	*Echium plantagineum*	39.013376	-7.255006
42	1	*Philaenus* sp.	F	4	*Lavatera cretica*	39.011178	-7.080551

Annex F – Kruskal-Wallis and Fisher's LSD tests

Table F.1 – Summary of abundance of different species of *Xylella fastidiosa* vectors and potential vectors (dependent variable) collected in Alentejo Region during spring of 2017 by 22 environmental factors (independent variable). N = number of samples in each class; Sum = total number of insect vectors; Mean = mean abundance of insect vectors; SD = standard deviation of insect vectors; SE = standard error of the mean. Presence of vectors highlighted in grey.

Dependent variable	Independent variable	Class	N	Sum	Mean	SD	SE
L. coleoptrata	Fam	Amaryllidaceae	1	0	0.0000	NA	NA
L. coleoptrata	Fam	Apiaceae	37	0	0.0000	0.0000	0.0000
L. coleoptrata	Fam	Asparagaceae	1	0	0.0000	NA	NA
L. coleoptrata	Fam	Asteraceae	57	0	0.0000	0.0000	0.0000
L. coleoptrata	Fam	Boraginaceae	18	0	0.0000	0.0000	0.0000
L. coleoptrata	Fam	Brassicaceae	5	0	0.0000	0.0000	0.0000
L. coleoptrata	Fam	Caryophyllaceae	1	0	0.0000	NA	NA
L. coleoptrata	Fam	Cistaceae	3	0	0.0000	0.0000	0.0000
L. coleoptrata	Fam	Convolvulaceae	11	2	0.1818	0.6030	0.1818
L. coleoptrata	Fam	Dipsacaceae	5	0	0.0000	0.0000	0.0000
L. coleoptrata	Fam	Fabaceae	3	0	0.0000	0.0000	0.0000
L. coleoptrata	Fam	Gentiaceae	2	0	0.0000	0.0000	0.0000
L. coleoptrata	Fam	Geraniaceae	1	0	0.0000	NA	NA
L. coleoptrata	Fam	Hypericaceae	2	0	0.0000	0.0000	0.0000
L. coleoptrata	Fam	Malvaceae	16	0	0.0000	0.0000	0.0000
L. coleoptrata	Fam	Papaveraceae	6	0	0.0000	0.0000	0.0000
L. coleoptrata	Fam	Plantaginaceae	1	0	0.0000	NA	NA
L. coleoptrata	Fam	Primulaceae	1	0	0.0000	NA	NA
L. coleoptrata	Fam	Ranunculaceae	1	0	0.0000	NA	NA
L. coleoptrata	Fam	Scrophulariaceae	5	2	0.4000	0.8944	0.4000
L. coleoptrata	Fam	Zygophyllaceae	1	0	0.0000	NA	NA
L. coleoptrata	Gen	*Allium*	1	0	0.0000	NA	NA
L. coleoptrata	Gen	*Ammi*	1	0	0.0000	NA	NA
L. coleoptrata	Gen	*Anacyclus*	8	0	0.0000	0.0000	0.0000
L. coleoptrata	Gen	*Anagallis*	1	0	0.0000	NA	NA
L. coleoptrata	Gen	*Anchusa*	1	0	0.0000	NA	NA
L. coleoptrata	Gen	*Andryala*	14	0	0.0000	0.0000	0.0000
L. coleoptrata	Gen	*Cachrys*	4	0	0.0000	0.0000	0.0000
L. coleoptrata	Gen	*Calendula*	1	0	0.0000	NA	NA
L. coleoptrata	Gen	*Carduus*	2	0	0.0000	0.0000	0.0000
L. coleoptrata	Gen	*Centaurium*	2	0	0.0000	0.0000	0.0000
L. coleoptrata	Gen	*Chamaemelum*	10	0	0.0000	0.0000	0.0000
L. coleoptrata	Gen	*Chrysanthemum*	5	0	0.0000	0.0000	0.0000
L. coleoptrata	Gen	*Cichorium*	3	0	0.0000	0.0000	0.0000
L. coleoptrata	Gen	*Cistus*	3	0	0.0000	0.0000	0.0000
L. coleoptrata	Gen	*Conium*	1	0	0.0000	NA	NA
L. coleoptrata	Gen	*Convolvulus*	11	2	0.1818	0.6030	0.1818
L. coleoptrata	Gen	*Conyza*	1	0	0.0000	NA	NA
L. coleoptrata	Gen	*Crepis*	5	0	0.0000	0.0000	0.0000
L. coleoptrata	Gen	*Daucus*	21	0	0.0000	0.0000	0.0000
L. coleoptrata	Gen	*Echium*	15	0	0.0000	0.0000	0.0000
L. coleoptrata	Gen	*Elaeoselinum*	2	0	0.0000	0.0000	0.0000
L. coleoptrata	Gen	*Erodium*	1	0	0.0000	NA	NA
L. coleoptrata	Gen	*Foeniculum*	3	0	0.0000	0.0000	0.0000
L. coleoptrata	Gen	*Galactites*	3	0	0.0000	0.0000	0.0000
L. coleoptrata	Gen	*Heliotropium*	2	0	0.0000	0.0000	0.0000
L. coleoptrata	Gen	*Hirschfeldia*	4	0	0.0000	0.0000	0.0000
L. coleoptrata	Gen	*Hypericum*	2	0	0.0000	0.0000	0.0000
L. coleoptrata	Gen	*Lavatera*	16	0	0.0000	0.0000	0.0000
L. coleoptrata	Gen	*Linaria*	1	0	0.0000	NA	NA
L. coleoptrata	Gen	*Mantisalca*	1	0	0.0000	NA	NA
L. coleoptrata	Gen	*Nigella*	1	0	0.0000	NA	NA

Table F.1 (cont.) – Summary of abundance of different species of *Xylella fastidiosa* vectors and potential vectors (dependent variable) collected in Alentejo Region during spring of 2017 by 22 environmental factors (independent variable). N = number of samples in each class; Sum = total number of insect vectors; Mean = mean abundance of insect vectors; SD = standard deviation of insect vectors; SE = standard error of the mean. Presence of vectors highlighted in grey.

Dependent variable	Independent variable	Class	N	Sum	Mean	SD	SE
L. coleoptrata	Gen	*Ononis*	3	0	0.0000	0.0000	0.0000
L. coleoptrata	Gen	*Ornithogalum*	1	0	0.0000	NA	NA
L. coleoptrata	Gen	*Papaver*	6	0	0.0000	0.0000	0.0000
L. coleoptrata	Gen	*Pulicaria*	1	0	0.0000	NA	NA
L. coleoptrata	Gen	*Raphanus*	1	0	0.0000	NA	NA
L. coleoptrata	Gen	*Ridolfia*	2	0	0.0000	0.0000	0.0000
L. coleoptrata	Gen	*Scabiosa*	5	0	0.0000	0.0000	0.0000
L. coleoptrata	Gen	*Scolymus*	1	0	0.0000	NA	NA
L. coleoptrata	Gen	*Spergularia*	1	0	0.0000	NA	NA
L. coleoptrata	Gen	*Tolpis*	1	0	0.0000	NA	NA
L. coleoptrata	Gen	*Torilis*	3	0	0.0000	0.0000	0.0000
L. coleoptrata	Gen	*Tribulus*	1	0	0.0000	NA	NA
L. coleoptrata	Gen	*Urospermum*	1	0	0.0000	NA	NA
L. coleoptrata	Gen	*Verbascum*	5	2	0.4000	0.8944	0.4000
L. coleoptrata	Spe	*Allium ampeloprasum*	1	0	0.0000	NA	NA
L. coleoptrata	Spe	*Ammi majus*	1	0	0.0000	NA	NA
L. coleoptrata	Spe	*Anacyclus radiatus*	8	0	0.0000	0.0000	0.0000
L. coleoptrata	Spe	*Anagallis arvensis*	1	0	0.0000	NA	NA
L. coleoptrata	Spe	*Anchusa azurea*	1	0	0.0000	NA	NA
L. coleoptrata	Spe	*Andryala integrifolia*	10	0	0.0000	0.0000	0.0000
L. coleoptrata	Spe	*Andryala laxiflora*	4	0	0.0000	0.0000	0.0000
L. coleoptrata	Spe	*Cachrys sicula*	4	0	0.0000	0.0000	0.0000
L. coleoptrata	Spe	*Calendula arvensis*	1	0	0.0000	NA	NA
L. coleoptrata	Spe	*Carduus tenuiflorus*	2	0	0.0000	0.0000	0.0000
L. coleoptrata	Spe	*Centaurium pulchellum*	2	0	0.0000	0.0000	0.0000
L. coleoptrata	Spe	*Chamaemelum mixtum*	10	0	0.0000	0.0000	0.0000
L. coleoptrata	Spe	*Chrysanthemum coronarium*	4	0	0.0000	0.0000	0.0000
L. coleoptrata	Spe	*Chrysanthemum segetum*	1	0	0.0000	NA	NA
L. coleoptrata	Spe	*Cichorium intybus*	3	0	0.0000	0.0000	0.0000
L. coleoptrata	Spe	*Cistus crispus*	1	0	0.0000	NA	NA
L. coleoptrata	Spe	*Cistus salvifolius*	2	0	0.0000	0.0000	0.0000
L. coleoptrata	Spe	*Conium maculatum*	1	0	0.0000	NA	NA
L. coleoptrata	Spe	*Convolvulus althaeoides*	2	0	0.0000	0.0000	0.0000
L. coleoptrata	Spe	*Convolvulus arvensis*	9	2	0.2222	0.6667	0.2222
L. coleoptrata	Spe	*Conyza bonariensis*	1	0	0.0000	NA	NA
L. coleoptrata	Spe	*Crepis capillaris*	3	0	0.0000	0.0000	0.0000
L. coleoptrata	Spe	*Crepis* sp.	1	0	0.0000	NA	NA
L. coleoptrata	Spe	*Crepis vesicaria*	1	0	0.0000	NA	NA
L. coleoptrata	Spe	*Daucus carota*	16	0	0.0000	0.0000	0.0000
L. coleoptrata	Spe	*Daucus crinitus*	1	0	0.0000	NA	NA
L. coleoptrata	Spe	*Daucus muricatus*	4	0	0.0000	0.0000	0.0000
L. coleoptrata	Spe	*Echium plantagineum*	15	0	0.0000	0.0000	0.0000
L. coleoptrata	Spe	*Elaeoselinum foetidum*	2	0	0.0000	0.0000	0.0000
L. coleoptrata	Spe	*Erodium moschatum*	1	0	0.0000	NA	NA
L. coleoptrata	Spe	*Foeniculum vulgare*	3	0	0.0000	0.0000	0.0000
L. coleoptrata	Spe	*Galactites tomentosus*	3	0	0.0000	0.0000	0.0000
L. coleoptrata	Spe	*Heliotropium europaeum*	2	0	0.0000	0.0000	0.0000
L. coleoptrata	Spe	*Hirschfeldia incana*	4	0	0.0000	0.0000	0.0000
L. coleoptrata	Spe	*Hypericum perforatum*	2	0	0.0000	0.0000	0.0000
L. coleoptrata	Spe	*Lavatera cretica*	13	0	0.0000	0.0000	0.0000
L. coleoptrata	Spe	*Lavatera trimestris*	3	0	0.0000	0.0000	0.0000
L. coleoptrata	Spe	*Linaria spartea*	1	0	0.0000	NA	NA
L. coleoptrata	Spe	*Mantisalca salmantica*	1	0	0.0000	NA	NA
L. coleoptrata	Spe	*Nigella damascena*	1	0	0.0000	NA	NA

Table F.1 (cont.) – Summary of abundance of different species of *Xylella fastidiosa* vectors and potential vectors (dependent variable) collected in Alentejo Region during spring of 2017 by 22 environmental factors (independent variable). N = number of samples in each class; Sum = total number of insect vectors; Mean = mean abundance of insect vectors; SD = standard deviation of insect vectors; SE = standard error of the mean. Presence of vectors highlighted in grey.

Dependent variable	Independent variable	Class	N	Sum	Mean	SD	SE
L. coleoptrata	Spe	*Ononis pubescens*	2	0	0.0000	0.0000	0.0000
L. coleoptrata	Spe	*Ononis viscosa*	1	0	0.0000	NA	NA
L. coleoptrata	Spe	*Ornithogalum narbonense*	1	0	0.0000	NA	NA
L. coleoptrata	Spe	*Papaver dubium*	1	0	0.0000	NA	NA
L. coleoptrata	Spe	*Papaver rhoeas*	5	0	0.0000	0.0000	0.0000
L. coleoptrata	Spe	*Pulicaria paludosa*	1	0	0.0000	NA	NA
L. coleoptrata	Spe	*Raphanus raphanistrum*	1	0	0.0000	NA	NA
L. coleoptrata	Spe	*Ridolfia segetum*	2	0	0.0000	0.0000	0.0000
L. coleoptrata	Spe	*Scabiosa atropurpurea*	5	0	0.0000	0.0000	0.0000
L. coleoptrata	Spe	*Scolymus hispanicus*	1	0	0.0000	NA	NA
L. coleoptrata	Spe	*Spergularia purpurea*	1	0	0.0000	NA	NA
L. coleoptrata	Spe	*Tolpis barbata*	1	0	0.0000	NA	NA
L. coleoptrata	Spe	*Torilis arvensis*	2	0	0.0000	0.0000	0.0000
L. coleoptrata	Spe	*Torilis sp.*	1	0	0.0000	NA	NA
L. coleoptrata	Spe	*Tribulus terrestris*	1	0	0.0000	NA	NA
L. coleoptrata	Spe	*Urospermum picroides*	1	0	0.0000	NA	NA
L. coleoptrata	Spe	*Verbascum sinuatum*	5	2	0.4000	0.8944	0.4000
L. coleoptrata	GU	0	8	0	0.0000	0.0000	0.0000
L. coleoptrata	GU	1	3	0	0.0000	0.0000	0.0000
L. coleoptrata	GU	2	14	0	0.0000	0.0000	0.0000
L. coleoptrata	GU	3	2	2	1	1,4142	1
L. coleoptrata	GU	4	2	0	0.0000	0.0000	0.0000
L. coleoptrata	GU	6	8	0	0.0000	0.0000	0.0000
L. coleoptrata	GU	7	2	0	0.0000	0.0000	0.0000
L. coleoptrata	GU	8	14	0	0.0000	0.0000	0.0000
L. coleoptrata	GU	9	14	0	0.0000	0.0000	0.0000
L. coleoptrata	GU	13	9	0	0.0000	0.0000	0.0000
L. coleoptrata	GU	14	7	0	0.0000	0.0000	0.0000
L. coleoptrata	GU	15	14	0	0.0000	0.0000	0.0000
L. coleoptrata	GU	19	9	0	0.0000	0.0000	0.0000
L. coleoptrata	GU	20	9	0	0.0000	0.0000	0.0000
L. coleoptrata	GU	21	8	2	0.2500	0.7071	0.2500
L. coleoptrata	GU	25	8	0	0.0000	0.0000	0.0000
L. coleoptrata	GU	26	9	0	0.0000	0.0000	0.0000
L. coleoptrata	GU	27	10	0	0.0000	0.0000	0.0000
L. coleoptrata	Host	Mixed ground cover	57	4	0.0702	0.3713	0.0492
L. coleoptrata	Host	Olive	93	0	0.0000	0.0000	0.0000
L. coleoptrata	DistWat	[0, 100]	6	0	0.0000	0.0000	0.0000
L. coleoptrata	DistWat	]100, 500]	26	0	0.0000	0.0000	0.0000
L. coleoptrata	DistWat	]500, 1000]	42	0	0.0000	0.0000	0.0000
L. coleoptrata	DistWat	]1000, 2000]	43	0	0.0000	0.0000	0.0000
L. coleoptrata	DistWat	> 2000	33	4	0.1212	0.4846	0.0844
L. coleoptrata	Alti	[0, 50]	7	0	0.0000	0.0000	0.0000
L. coleoptrata	Alti	]50, 100]	8	0	0.0000	0.0000	0.0000
L. coleoptrata	Alti	]100, 200]	61	2	0.0328	0.2561	0.0328
L. coleoptrata	Alti	]200, 300]	53	0	0.0000	0.0000	0.0000
L. coleoptrata	Alti	> 300	21	2	0.0952	0.4364	0.0952
L. coleoptrata	Asp	Flat	2	0	0.0000	0.0000	0.0000
L. coleoptrata	Asp	North: [0, 45] ∪]316, 360]	48	4	0.0833	0.4039	0.0583
L. coleoptrata	Asp	East:]45, 135]	29	0	0.0000	0.0000	0.0000
L. coleoptrata	Asp	South:]135, 225]	34	0	0.0000	0.0000	0.0000
L. coleoptrata	Asp	West:]225, 315]	37	0	0.0000	0.0000	0.0000
L. coleoptrata	Tmed	19	30	0	0.0000	0.0000	0.0000
L. coleoptrata	Tmed	21	67	2	0.0299	0.2443	0.0299

Table F.1 (cont.) – Summary of abundance of different species of *Xylella fastidiosa* vectors and potential vectors (dependent variable) collected in Alentejo Region during spring of 2017 by 22 environmental factors (independent variable). N = number of samples in each class; Sum = total number of insect vectors; Mean = mean abundance of insect vectors; SD = standard deviation of insect vectors; SE = standard error of the mean. Presence of vectors highlighted in grey.

Dependent variable	Independent variable	Class	N	Sum	Mean	SD	SE
L. coleoptrata	Tmed	24	14	0	0.0000	0.0000	0.0000
L. coleoptrata	Tmed	26	38	2	0.0526	0.3244	0.0526
L. coleoptrata	Tmed	28	1	0	0.0000	NA	NA
L. coleoptrata	Prec	5	33	0	0.0000	0.0000	0.0000
L. coleoptrata	Prec	10	20	2	0.1000	0.4472	0.1000
L. coleoptrata	Prec	25	38	2	0.0526	0.3244	0.0526
L. coleoptrata	Prec	50	59	0	0.0000	0.0000	0.0000
L. coleoptrata	OlivDist	[0, 50]	62	2	0.0323	0.2540	0.0323
L. coleoptrata	OlivDist	]50, 100]	25	0	0.0000	0.0000	0.0000
L. coleoptrata	OlivDist	]100, 250]	28	2	0.0714	0.3780	0.0714
L. coleoptrata	OlivDist	]250, 1000]	30	0	0.0000	0.0000	0.0000
L. coleoptrata	OlivDist	> 1000	5	0	0.0000	0.0000	0.0000
L. coleoptrata	Oliv250	0	37	0	0.0000	0.0000	0.0000
L. coleoptrata	Oliv250	]0, 25]	47	2	0.0426	0.2917	0.0426
L. coleoptrata	Oliv250	]25, 50]	29	2	0.0690	0.3714	0.069
L. coleoptrata	Oliv250	]50, 75]	17	0	0.0000	0.0000	0.0000
L. coleoptrata	Oliv250	]75, 100]	17	0	0.0000	0.0000	0.0000
L. coleoptrata	Oliv250	100	3	0	0.0000	0.0000	0.0000
L. coleoptrata	Oliv500	0	19	0	0.0000	0.0000	0.0000
L. coleoptrata	Oliv500	]0, 25]	68	4	0.0588	0.3404	0.0413
L. coleoptrata	Oliv500	]25, 50]	34	0	0.0000	0.0000	0.0000
L. coleoptrata	Oliv500	]50, 75]	22	0	0.0000	0.0000	0.0000
L. coleoptrata	Oliv500	]75, 100]	7	0	0.0000	0.0000	0.0000
L. coleoptrata	Oliv500	100	0	-	-	-	-
L. coleoptrata	Oliv1000	0	9	0	0.0000	0.0000	0.0000
L. coleoptrata	Oliv1000	]0, 25]	83	2	0.0241	0.2195	0.0241
L. coleoptrata	Oliv1000	]25, 50]	40	2	0.0500	0.3162	0.0500
L. coleoptrata	Oliv1000	]50, 75]	17	0	0.0000	0.0000	0.0000
L. coleoptrata	Oliv1000	]75, 100]	1	0	0.0000	NA	NA
L. coleoptrata	Oliv1000	100	0	-	-	-	-
L. coleoptrata	RipDist	[0, 50]	2	0	0.0000	0.0000	0.0000
L. coleoptrata	RipDist	]50, 100]	0	-	-	-	-
L. coleoptrata	RipDist	]100, 250]	1	0	0.0000	NA	NA
L. coleoptrata	RipDist	]250, 1000]	27	0	0.0000	0.0000	0.0000
L. coleoptrata	RipDist	> 1000	120	4	0.0333	0.2571	0.0235
L. coleoptrata	Rip250	0	145	4	0.0276	0.2341	0.0194
L. coleoptrata	Rip250	]0, 25]	5	0	0.0000	0.0000	0.0000
L. coleoptrata	Rip250	]25, 50]	0	-	-	-	-
L. coleoptrata	Rip250	]50, 75]	0	-	-	-	-
L. coleoptrata	Rip250	]75, 100]	0	-	-	-	-
L. coleoptrata	Rip250	100	0	-	-	-	-
L. coleoptrata	Rip500	0	137	4	0.0292	0.2408	0.0206
L. coleoptrata	Rip500	]0, 25]	13	0	0.0000	0.0000	0.0000
L. coleoptrata	Rip500	]25, 50]	0	-	-	-	-
L. coleoptrata	Rip500	]50, 75]	0	-	-	-	-
L. coleoptrata	Rip500	]75, 100]	0	-	-	-	-
L. coleoptrata	Rip500	100	0	-	-	-	-
L. coleoptrata	Rip1000	0	122	4	0.0328	0.2550	0.0231
L. coleoptrata	Rip1000	]0, 25]	28	0	0.0000	0.0000	0.0000
L. coleoptrata	Rip1000	]25, 50]	0	-	-	-	-
L. coleoptrata	Rip1000	]50, 75]	0	-	-	-	-
L. coleoptrata	Rip1000	]75, 100]	0	-	-	-	-
L. coleoptrata	Rip1000	100	0	-	-	-	-

Table F.1 (cont.) – Summary of abundance of different species of *Xylella fastidiosa* vectors and potential vectors (dependent variable) collected in Alentejo Region during spring of 2017 by 22 environmental factors (independent variable). N = number of samples in each class; Sum = total number of insect vectors; Mean = mean abundance of insect vectors; SD = standard deviation of insect vectors; SE = standard error of the mean. Presence of vectors highlighted in grey

Dependent variable	Independent variable	Class	N	Sum	Mean	SD	SE
L. coleoptrata	Vine250	0	133	4	0.0301	0.2443	0.0212
L. coleoptrata	Vine250	]0, 25]	13	0	0.0000	0.0000	0.0000
L. coleoptrata	Vine250	]25, 50]	4	0	0.0000	0.0000	0.0000
L. coleoptrata	Vine250	]50, 75]	0	-	-	-	-
L. coleoptrata	Vine250	]75, 100]	0	-	-	-	-
L. coleoptrata	Vine250	100	0	-	-	-	-
L. coleoptrata	Past250	0	70	2	0.0286	0.2390	0.0286
L. coleoptrata	Past250	]0, 25]	58	2	0.0345	0.2626	0.0345
L. coleoptrata	Past250	]25, 50]	16	0	0.0000	0.0000	0.0000
L. coleoptrata	Past250	]50, 75]	6	0	0.0000	0.0000	0.0000
L. coleoptrata	Past250	]75, 100]	0	-	-	-	-
L. coleoptrata	Past250	100	0	-	-	-	-
L. coleoptrata	Holm250	0	114	4	0.0351	0.2637	0.0247
L. coleoptrata	Holm250	]0, 25]	26	0	0.0000	0.0000	0.0000
L. coleoptrata	Holm250	]25, 50]	2	0	0.0000	0.0000	0.0000
L. coleoptrata	Holm250	]50, 75]	6	0	0.0000	0.0000	0.0000
L. coleoptrata	Holm250	]75, 100]	2	0	0.0000	0.0000	0.0000
L. coleoptrata	Holm250	100	0	-	-	-	-
L. coleoptrata	Cork250	0	122	4	0.0328	0.2550	0.0231
L. coleoptrata	Cork250	]0, 25]	25	0	0.0000	0.0000	0.0000
L. coleoptrata	Cork250	]25, 50]	3	0	0.0000	0.0000	0.0000
L. coleoptrata	Cork250	]50, 75]	0	0	0.0000	-	-
L. coleoptrata	Cork250	]75, 100]	0	0	0.0000	-	-
L. coleoptrata	Cork250	100	0	0	0.0000	-	-
N. campestris	Fam	Amaryllidaceae	1	0	0.0000	NA	NA
N. campestris	Fam	Apiaceae	37	0	0.0000	0.0000	0.0000
N. campestris	Fam	Asparagaceae	1	0	0.0000	NA	NA
N. campestris	Fam	Asteraceae	57	0	0.0000	0.0000	0.0000
N. campestris	Fam	Boraginaceae	18	0	0.0000	0.0000	0.0000
N. campestris	Fam	Brassicaceae	5	0	0.0000	0.0000	0.0000
N. campestris	Fam	Caryophyllaceae	1	0	0.0000	NA	NA
N. campestris	Fam	Cistaceae	3	0	0.0000	0.0000	0.0000
N. campestris	Fam	Convolvulaceae	11	1	0.0909	0.3015	0.0909
N. campestris	Fam	Dipsacaceae	5	0	0.0000	0.0000	0.0000
N. campestris	Fam	Fabaceae	3	0	0.0000	0.0000	0.0000
N. campestris	Fam	Gentiaceae	2	0	0.0000	0.0000	0.0000
N. campestris	Fam	Geraniaceae	1	0	0.0000	NA	NA
N. campestris	Fam	Hypericaceae	2	0	0.0000	0.0000	0.0000
N. campestris	Fam	Malvaceae	16	0	0.0000	0.0000	0.0000
N. campestris	Fam	Papaveraceae	6	0	0.0000	0.0000	0.0000
N. campestris	Fam	Plantaginaceae	1	0	0.0000	NA	NA
N. campestris	Fam	Primulaceae	1	0	0.0000	NA	NA
N. campestris	Fam	Ranunculaceae	1	0	0.0000	NA	NA
N. campestris	Fam	Scrophulariaceae	5	0	0.0000	0.0000	0.0000
N. campestris	Fam	Zygophyllaceae	1	0	0.0000	NA	NA
N. campestris	Gen	*Allium*	1	0	0.0000	NA	NA
N. campestris	Gen	*Ammi*	1	0	0.0000	NA	NA
N. campestris	Gen	*Anacyclus*	8	0	0.0000	0.0000	0.0000
N. campestris	Gen	*Anagallis*	1	0	0.0000	NA	NA
N. campestris	Gen	*Anchusa*	1	0	0.0000	NA	NA
N. campestris	Gen	*Andryala*	14	0	0.0000	0.0000	0.0000
N. campestris	Gen	*Cachrys*	4	0	0.0000	0.0000	0.0000
N. campestris	Gen	*Calendula*	1	0	0.0000	NA	NA
N. campestris	Gen	*Carduus*	2	0	0.0000	0.0000	0.0000
N. campestris	Gen	*Centaurium*	2	0	0.0000	0.0000	0.0000

Table F.1 (cont.) – Summary of abundance of different species of *Xylella fastidiosa* vectors and potential vectors (dependent variable) collected in Alentejo Region during spring of 2017 by 22 environmental factors (independent variable). N = number of samples in each class; Sum = total number of insect vectors; Mean = mean abundance of insect vectors; SD = standard deviation of insect vectors; SE = standard error of the mean. Presence of vectors highlighted in grey

Dependent variable	Independent variable	Class	N	Sum	Mean	SD	SE
N. campestris	Gen	*Chamaemelum*	10	0	0.0000	0.0000	0.0000
N. campestris	Gen	*Chrysanthemum*	5	0	0.0000	0.0000	0.0000
N. campestris	Gen	*Cichorium*	3	0	0.0000	0.0000	0.0000
N. campestris	Gen	*Cistus*	3	0	0.0000	0.0000	0.0000
N. campestris	Gen	*Conium*	1	0	0.0000	NA	NA
N. campestris	Gen	*Convolvulus*	11	1	0.0909	0.3015	0.0909
N. campestris	Gen	*Conyza*	1	0	0.0000	NA	NA
N. campestris	Gen	*Crepis*	5	0	0.0000	0.0000	0.0000
N. campestris	Gen	*Daucus*	21	0	0.0000	0.0000	0.0000
N. campestris	Gen	*Echium*	15	0	0.0000	0.0000	0.0000
N. campestris	Gen	*Elaeoselinum*	2	0	0.0000	0.0000	0.0000
N. campestris	Gen	*Erodium*	1	0	0.0000	NA	NA
N. campestris	Gen	*Foeniculum*	3	0	0.0000	0.0000	0.0000
N. campestris	Gen	*Galactites*	3	0	0.0000	0.0000	0.0000
N. campestris	Gen	*Heliotropium*	2	0	0.0000	0.0000	0.0000
N. campestris	Gen	*Hirschfeldia*	4	0	0.0000	0.0000	0.0000
N. campestris	Gen	*Hypericum*	2	0	0.0000	0.0000	0.0000
N. campestris	Gen	*Lavatera*	16	0	0.0000	0.0000	0.0000
N. campestris	Gen	*Linaria*	1	0	0.0000	NA	NA
N. campestris	Gen	*Mantisalca*	1	0	0.0000	NA	NA
N. campestris	Gen	*Nigella*	1	0	0.0000	NA	NA
N. campestris	Gen	*Ononis*	3	0	0.0000	0.0000	0.0000
N. campestris	Gen	*Ornithogalum*	1	0	0.0000	NA	NA
N. campestris	Gen	*Papaver*	6	0	0.0000	0.0000	0.0000
N. campestris	Gen	*Pulicaria*	1	0	0.0000	NA	NA
N. campestris	Gen	*Raphanus*	1	0	0.0000	NA	NA
N. campestris	Gen	*Ridolfia*	2	0	0.0000	0.0000	0.0000
N. campestris	Gen	*Scabiosa*	5	0	0.0000	0.0000	0.0000
N. campestris	Gen	*Scolymus*	1	0	0.0000	NA	NA
N. campestris	Gen	*Spergularia*	1	0	0.0000	NA	NA
N. campestris	Gen	*Tolpis*	1	0	0.0000	NA	NA
N. campestris	Gen	*Torilis*	3	0	0.0000	0.0000	0.0000
N. campestris	Gen	*Tribulus*	1	0	0.0000	NA	NA
N. campestris	Gen	*Urospermum*	1	0	0.0000	NA	NA
N. campestris	Gen	*Verbascum*	5	0	0.0000	0.0000	0.0000
N. campestris	Spe	*Allium ampeloprasum*	1	0	0.0000	NA	NA
N. campestris	Spe	*Ammi majus*	1	0	0.0000	NA	NA
N. campestris	Spe	*Anacyclus radiatus*	8	0	0.0000	0.0000	0.0000
N. campestris	Spe	*Anagallis arvensis*	1	0	0.0000	NA	NA
N. campestris	Spe	*Anchusa azurea*	1	0	0.0000	NA	NA
N. campestris	Spe	*Andryala integrifolia*	10	0	0.0000	0.0000	0.0000
N. campestris	Spe	*Andryala laxiflora*	4	0	0.0000	0.0000	0.0000
N. campestris	Spe	*Cachrys sicula*	4	0	0.0000	0.0000	0.0000
N. campestris	Spe	*Calendula arvensis*	1	0	0.0000	NA	NA
N. campestris	Spe	*Carduus tenuiflorus*	2	0	0.0000	0.0000	0.0000
N. campestris	Spe	*Centaurium pulchellum*	2	0	0.0000	0.0000	0.0000
N. campestris	Spe	*Chamaemelum mixtum*	10	0	0.0000	0.0000	0.0000
N. campestris	Spe	*Chrysanthemum coronarium*	4	0	0.0000	0.0000	0.0000
N. campestris	Spe	*Chrysanthemum segetum*	1	0	0.0000	NA	NA
N. campestris	Spe	*Cichorium intybus*	3	0	0.0000	0.0000	0.0000
N. campestris	Spe	*Cistus crispus*	1	0	0.0000	NA	NA
N. campestris	Spe	*Cistus salvifolius*	2	0	0.0000	0.0000	0.0000
N. campestris	Spe	*Conium maculatum*	1	0	0.0000	NA	NA
N. campestris	Spe	*Convolvulus althaeoides*	2	0	0.0000	0.0000	0.0000

Table F.1 (cont.) – Summary of abundance of different species of *Xylella fastidiosa* vectors and potential vectors (dependent variable) collected in Alentejo Region during spring of 2017 by 22 environmental factors (independent variable). N = number of samples in each class; Sum = total number of insect vectors; Mean = mean abundance of insect vectors; SD = standard deviation of insect vectors; SE = standard error of the mean. Presence of vectors highlighted in grey

Dependent variable	Independent variable	Class	N	Sum	Mean	SD	SE
N. campestris	Spe	*Convolvulus arvensis*	9	1	0.1111	0.3333	0.1111
N. campestris	Spe	*Conyza bonariensis*	1	0	0.0000	NA	NA
N. campestris	Spe	*Crepis capillaris*	3	0	0.0000	0.0000	0.0000
N. campestris	Spe	*Crepis sp.*	1	0	0.0000	NA	NA
N. campestris	Spe	*Crepis vesicaria*	1	0	0.0000	NA	NA
N. campestris	Spe	*Daucus carota*	16	0	0.0000	0.0000	0.0000
N. campestris	Spe	*Daucus crinitus*	1	0	0.0000	NA	NA
N. campestris	Spe	*Daucus muricatus*	4	0	0.0000	0.0000	0.0000
N. campestris	Spe	*Echium plantagineum*	15	0	0.0000	0.0000	0.0000
N. campestris	Spe	*Elaeoselinum foetidum*	2	0	0.0000	0.0000	0.0000
N. campestris	Spe	*Erodium moschatum*	1	0	0.0000	NA	NA
N. campestris	Spe	*Foeniculum vulgare*	3	0	0.0000	0.0000	0.0000
N. campestris	Spe	*Galactites tomentosus*	3	0	0.0000	0.0000	0.0000
N. campestris	Spe	*Heliotropium europaeum*	2	0	0.0000	0.0000	0.0000
N. campestris	Spe	*Hirschfeldia incana*	4	0	0.0000	0.0000	0.0000
N. campestris	Spe	*Hypericum perforatum*	2	0	0.0000	0.0000	0.0000
N. campestris	Spe	*Lavatera cretica*	13	0	0.0000	0.0000	0.0000
N. campestris	Spe	*Lavatera trimestris*	3	0	0.0000	0.0000	0.0000
N. campestris	Spe	*Linaria spartea*	1	0	0.0000	NA	NA
N. campestris	Spe	*Mantisalca salmantica*	1	0	0.0000	NA	NA
N. campestris	Spe	*Nigella damascena*	1	0	0.0000	NA	NA
N. campestris	Spe	*Ononis pubescens*	2	0	0.0000	0.0000	0.0000
N. campestris	Spe	*Ononis viscosa*	1	0	0.0000	NA	NA
N. campestris	Spe	*Ornithogalum narbonense*	1	0	0.0000	NA	NA
N. campestris	Spe	*Papaver dubium*	1	0	0.0000	NA	NA
N. campestris	Spe	*Papaver rhoeas*	5	0	0.0000	0.0000	0.0000
N. campestris	Spe	*Pulicaria paludosa*	1	0	0.0000	NA	NA
N. campestris	Spe	*Raphanus raphanistrum*	1	0	0.0000	NA	NA
N. campestris	Spe	*Ridolfia segetum*	2	0	0.0000	0.0000	0.0000
N. campestris	Spe	*Scabiosa atropurpurea*	5	0	0.0000	0.0000	0.0000
N. campestris	Spe	*Scolymus hispanicus*	1	0	0.0000	NA	NA
N. campestris	Spe	*Spergularia purpurea*	1	0	0.0000	NA	NA
N. campestris	Spe	*Tolpis barbata*	1	0	0.0000	NA	NA
N. campestris	Spe	*Torilis arvensis*	2	0	0.0000	0.0000	0.0000
N. campestris	Spe	*Torilis sp.*	1	0	0.0000	NA	NA
N. campestris	Spe	*Tribulus terrestris*	1	0	0.0000	NA	NA
N. campestris	Spe	*Urospermum picroides*	1	0	0.0000	NA	NA
N. campestris	Spe	*Verbascum sinuatum*	5	0	0.0000	0.0000	0.0000
N. campestris	GU	0	8	1	0.1250	0.3536	0.1250
N. campestris	GU	1	3	0	0.0000	0.0000	0.0000
N. campestris	GU	2	14	0	0.0000	0.0000	0.0000
N. campestris	GU	3	2	0	0.0000	0.0000	0.0000
N. campestris	GU	4	2	0	0.0000	0.0000	0.0000
N. campestris	GU	6	8	0	0.0000	0.0000	0.0000
N. campestris	GU	7	2	0	0.0000	0.0000	0.0000
N. campestris	GU	8	14	1	0.0714	0.2673	0.0714
N. campestris	GU	9	14	0	0.0000	0.0000	0.0000
N. campestris	GU	13	9	0	0.0000	0.0000	0.0000
N. campestris	GU	14	7	0	0.0000	0.0000	0.0000
N. campestris	GU	15	14	0	0.0000	0.0000	0.0000
N. campestris	GU	19	9	0	0.0000	0.0000	0.0000
N. campestris	GU	20	9	1	0.1111	0.3333	0.1111
N. campestris	GU	21	8	0	0.0000	0.0000	0.0000
N. campestris	GU	25	8	1	0.1250	0.3536	0.1250

Table F.1 (cont.) – Summary of abundance of different species of *Xylella fastidiosa* vectors and potential vectors (dependent variable) collected in Alentejo Region during spring of 2017 by 22 environmental factors (independent variable). N = number of samples in each class; Sum = total number of insect vectors; Mean = mean abundance of insect vectors; SD = standard deviation of insect vectors; SE = standard error of the mean. Presence of vectors highlighted in grey

Dependent variable	Independent variable	Class	N	Sum	Mean	SD	SE
N. campestris	GU	26	9	1	0.1111	0.3333	0.1111
N. campestris	GU	27	10	0	0.0000	0.0000	0.0000
N. campestris	Host	Mixed ground cover	57	1	0.0175	0.1325	0.0175
N. campestris	Host	Olive	93	4	0.0430	0.2040	0.0212
N. campestris	DistWat	[0, 100]	6	1	0.1667	0.4082	0.1667
N. campestris	DistWat	]100, 500]	26	0	0.0000	0.0000	0.0000
N. campestris	DistWat	]500, 1000]	42	2	0.0476	0.2155	0.0333
N. campestris	DistWat	]1000, 2000]	43	0	0.0000	0.0000	0.0000
N. campestris	DistWat	> 2000	33	2	0.0606	0.2423	0.0422
N. campestris	Alti	[0, 50]	7	1	0.1429	0.3780	0.1429
N. campestris	Alti	]50, 100]	8	0	0.0000	0.0000	0.0000
N. campestris	Alti	]100, 200]	61	3	0.0492	0.2180	0.0279
N. campestris	Alti	]200, 300]	53	0	0.0000	0.0000	0.0000
N. campestris	Alti	> 300	21	1	0.0476	0.2182	0.0476
N. campestris	Asp	Flat	2	0	0.0000	0.0000	0.0000
N. campestris	Asp	North: [0, 45] ∪]316, 360]	48	1	0.0208	0.1443	0.0208
N. campestris	Asp	East:]45, 135]	29	2	0.0690	0.2579	0.0479
N. campestris	Asp	South:]135, 225]	34	1	0.0294	0.1715	0.0294
N. campestris	Asp	West:]225, 315]	37	1	0.0270	0.1644	0.0270
N. campestris	Tmed	19	30	3	0.1000	0.3051	0.0557
N. campestris	Tmed	21	67	0	0.0000	0.0000	0.0000
N. campestris	Tmed	24	14	1	0.0714	0.2673	0.0714
N. campestris	Tmed	26	38	1	0.0263	0.1622	0.0263
N. campestris	Tmed	28	1	0	0.0000	NA	NA
N. campestris	Prec	5	33	1	0.0303	0.1741	0.0303
N. campestris	Prec	10	20	1	0.0500	0.2236	0.0500
N. campestris	Prec	25	38	2	0.0526	0.2263	0.0367
N. campestris	Prec	50	59	1	0.0169	0.1302	0.0169
N. campestris	OlivDist	[0, 50]	62	1	0.0161	0.1270	0.0161
N. campestris	OlivDist	]50, 100]	25	1	0.0400	0.2000	0.0400
N. campestris	OlivDist	]100, 250]	28	3	0.1071	0.3150	0.0595
N. campestris	OlivDist	]250, 1000]	30	0	0.0000	0.0000	0.0000
N. campestris	OlivDist	> 1000	5	0	0.0000	0.0000	0.0000
N. campestris	Oliv250	0	37	2	0.0541	0.2292	0.0377
N. campestris	Oliv250	]0, 25]	47	2	0.0426	0.2040	0.0298
N. campestris	Oliv250	]25, 50]	29	1	0.0345	0.1857	0.0345
N. campestris	Oliv250	]50, 75]	17	0	0.0000	0.0000	0.0000
N. campestris	Oliv250	]75, 100]	17	0	0.0000	0.0000	0.0000
N. campestris	Oliv250	100	3	0	0.0000	0.0000	0.0000
N. campestris	Oliv500	0	19	0	0.0000	0.0000	0.0000
N. campestris	Oliv500	]0, 25]	68	4	0.0588	0.2370	0.0287
N. campestris	Oliv500	]25, 50]	34	1	0.0294	0.1715	0.0294
N. campestris	Oliv500	]50, 75]	22	0	0.0000	0.0000	0.0000
N. campestris	Oliv500	]75, 100]	7	0	0.0000	0.0000	0.0000
N. campestris	Oliv500	100	0	-	-	-	-
N. campestris	Oliv1000	0	9	0	0.0000	0.0000	0.0000
N. campestris	Oliv1000	]0, 25]	83	4	0.0482	0.2155	0.0237
N. campestris	Oliv1000	]25, 50]	40	0	0.0000	0.0000	0.0000
N. campestris	Oliv1000	]50, 75]	17	1	0.0588	0.2425	0.0588
N. campestris	Oliv1000	]75, 100]	1	0	0.0000	NA	NA
N. campestris	Oliv1000	100	0	-	-	-	-
N. campestris	RipDist	[0, 50]	2	0	0.0000	0.0000	0.0000
N. campestris	RipDist	]50, 100]	0	-	-	-	-
N. campestris	RipDist	]100, 250]	1	0	0.0000	NA	NA

Table F.1 (cont.) – Summary of abundance of different species of *Xylella fastidiosa* vectors and potential vectors (dependent variable) collected in Alentejo Region during spring of 2017 by 22 environmental factors (independent variable). N = number of samples in each class; Sum = total number of insect vectors; Mean = mean abundance of insect vectors; SD = standard deviation of insect vectors; SE = standard error of the mean. Presence of vectors highlighted in grey

Dependent variable	Independent variable	Class	N	Sum	Mean	SD	SE
N. campestris	RipDist	]250, 1000]	27	1	0.0370	0.1925	0.0370
N. campestris	RipDist	> 1000	120	4	0.0333	0.1803	0.0165
N. campestris	Rip250	0	145	5	0.0345	0.1831	0.0152
N. campestris	Rip250	]0, 25]	5	0	0.0000	0.0000	0.0000
N. campestris	Rip250	]25, 50]	0	-	-	-	-
N. campestris	Rip250	]50, 75]	0	-	-	-	-
N. campestris	Rip250	]75, 100]	0	-	-	-	-
N. campestris	Rip250	100	0	-	-	-	-
N. campestris	Rip500	0	137	5	0.0365	0.1882	0.0161
N. campestris	Rip500	]0, 25]	13	0	0.0000	0.0000	0.0000
N. campestris	Rip500	]25, 50]	0	-	-	-	-
N. campestris	Rip500	]50, 75]	0	-	-	-	-
N. campestris	Rip500	]75, 100]	0	-	-	-	-
N. campestris	Rip500	100	0	-	-	-	-
N. campestris	Rip1000	0	122	4	0.0328	0.1788	0.0162
N. campestris	Rip1000	]0, 25]	28	1	0.0357	0.1890	0.0357
N. campestris	Rip1000	]25, 50]	0	-	-	-	-
N. campestris	Rip1000	]50, 75]	0	-	-	-	-
N. campestris	Rip1000	]75, 100]	0	-	-	-	-
N. campestris	Rip1000	100	0	-	-	-	-
N. campestris	Vine250	0	133	4	0.0301	0.1714	0.0149
N. campestris	Vine250	]0, 25]	13	0	0.0000	0.0000	0.0000
N. campestris	Vine250	]25, 50]	4	1	0.2500	0.5000	0.2500
N. campestris	Vine250	]50, 75]	0	-	-	-	-
N. campestris	Vine250	]75, 100]	0	-	-	-	-
N. campestris	Vine250	100	0	-	-	-	-
N. campestris	Past250	0	70	1	0.0143	0.1195	0.0143
N. campestris	Past250	]0, 25]	58	4	0.0690	0.2556	0.0336
N. campestris	Past250	]25, 50]	16	0	0.0000	0.0000	0.0000
N. campestris	Past250	]50, 75]	6	0	0.0000	0.0000	0.0000
N. campestris	Past250	]75, 100]	0	-	-	-	-
N. campestris	Past250	100	0	-	-	-	-
N. campestris	Holm250	0	114	3	0.0263	0.1608	0.0151
N. campestris	Holm250	]0, 25]	26	2	0.0769	0.2717	0.0533
N. campestris	Holm250	]25, 50]	2	0	0.0000	0.0000	0.0000
N. campestris	Holm250	]50, 75]	6	0	0.0000	0.0000	0.0000
N. campestris	Holm250	]75, 100]	2	0	0.0000	0.0000	0.0000
N. campestris	Holm250	100	0	-	-	-	-
N. campestris	Cork250	0	122	2	0.0164	0.1275	0.0115
N. campestris	Cork250	]0, 25]	25	3	0.1200	0.3317	0.0663
N. campestris	Cork250	]25, 50]	3	0	0.0000	0.0000	0.0000
N. campestris	Cork250	]50, 75]	0	-	-	-	-
N. campestris	Cork250	]75, 100]	0	-	-	-	-
N. campestris	Cork250	100	0	-	-	-	-
Philaenus sp.	Fam	Amaryllidaceae	1	0	0.0000	NA	NA
Philaenus sp.	Fam	Apiaceae	37	3	0.0811	0.2767	0.0455
Philaenus sp.	Fam	Asparagaceae	1	0	0.0000	NA	NA
Philaenus sp.	Fam	Asteraceae	57	4	0.0702	0.2577	0.0341
Philaenus sp.	Fam	Boraginaceae	18	2	0.1111	0.4714	0.1111
Philaenus sp.	Fam	Brassicaceae	5	0	0.0000	0.0000	0.0000
Philaenus sp.	Fam	Caryophyllaceae	1	0	0.0000	NA	NA
Philaenus sp.	Fam	Cistaceae	3	0	0.0000	0.0000	0.0000
Philaenus sp.	Fam	Convolvulaceae	11	0	0.0000	0.0000	0.0000
Philaenus sp.	Fam	Dipsacaceae	5	1	0.2000	0.4472	0.2000

Table F.1 (cont.) – Summary of abundance of different species of *Xylella fastidiosa* vectors and potential vectors (dependent variable) collected in Alentejo Region during spring of 2017 by 22 environmental factors (independent variable). N = number of samples in each class; Sum = total number of insect vectors; Mean = mean abundance of insect vectors; SD = standard deviation of insect vectors; SE = standard error of the mean. Presence of vectors highlighted in grey

Dependent variable	Independent variable	Class	N	Sum	Mean	SD	SE
Philaenus sp.	Fam	Fabaceae	3	0	0.0000	0.0000	0.0000
Philaenus sp.	Fam	Gentiaceae	2	0	0.0000	0.0000	0.0000
Philaenus sp.	Fam	Geraniaceae	1	0	0.0000	NA	NA
Philaenus sp.	Fam	Hypericaceae	2	0	0.0000	0.0000	0.0000
Philaenus sp.	Fam	Malvaceae	16	1	0.0625	0.2500	0.0625
Philaenus sp.	Fam	Papaveraceae	6	0	0.0000	0.0000	0.0000
Philaenus sp.	Fam	Plantaginaceae	1	0	0.0000	NA	NA
Philaenus sp.	Fam	Primulaceae	1	0	0.0000	NA	NA
Philaenus sp.	Fam	Ranunculaceae	1	0	0.0000	NA	NA
Philaenus sp.	Fam	Scrophulariaceae	5	0	0.0000	0.0000	0.0000
Philaenus sp.	Fam	Zygophyllaceae	1	0	0.0000	NA	NA
Philaenus sp.	Gen	*Allium*	1	0	0.0000	NA	NA
Philaenus sp.	Gen	*Ammi*	1	0	0.0000	NA	NA
Philaenus sp.	Gen	*Anacyclus*	8	0	0.0000	0.0000	0.0000
Philaenus sp.	Gen	*Anagallis*	1	0	0.0000	NA	NA
Philaenus sp.	Gen	*Anchusa*	1	0	0.0000	NA	NA
Philaenus sp.	Gen	*Andryala*	14	2	0.1429	0.3631	0.0971
Philaenus sp.	Gen	*Cachrys*	4	0	0.0000	0.0000	0.0000
Philaenus sp.	Gen	*Calendula*	1	0	0.0000	NA	NA
Philaenus sp.	Gen	*Carduus*	2	0	0.0000	0.0000	0.0000
Philaenus sp.	Gen	*Centaurium*	2	0	0.0000	0.0000	0.0000
Philaenus sp.	Gen	*Chamaemelum*	10	0	0.0000	0.0000	0.0000
Philaenus sp.	Gen	*Chrysanthemum*	5	0	0.0000	0.0000	0.0000
Philaenus sp.	Gen	*Cichorium*	3	0	0.0000	0.0000	0.0000
Philaenus sp.	Gen	*Cistus*	3	0	0.0000	0.0000	0.0000
Philaenus sp.	Gen	*Conium*	1	0	0.0000	NA	NA
Philaenus sp.	Gen	*Convolvulus*	11	0	0.0000	0.0000	0.0000
Philaenus sp.	Gen	*Conyza*	1	0	0.0000	NA	NA
Philaenus sp.	Gen	*Crepis*	5	0	0.0000	0.0000	0.0000
Philaenus sp.	Gen	*Daucus*	21	2	0.0952	0.3008	0.0656
Philaenus sp.	Gen	*Echium*	15	2	0.1333	0.5164	0.1333
Philaenus sp.	Gen	*Elaeoselinum*	2	0	0.0000	0.0000	0.0000
Philaenus sp.	Gen	*Erodium*	1	0	0.0000	NA	NA
Philaenus sp.	Gen	*Foeniculum*	3	1	0.3333	0.5774	0.3333
Philaenus sp.	Gen	*Galactites*	3	2	0.6667	0.5774	0.3333
Philaenus sp.	Gen	*Heliotropium*	2	0	0.0000	0.0000	0.0000
Philaenus sp.	Gen	*Hirschfeldia*	4	0	0.0000	0.0000	0.0000
Philaenus sp.	Gen	*Hypericum*	2	0	0.0000	0.0000	0.0000
Philaenus sp.	Gen	*Lavatera*	16	1	0.0625	0.2500	0.0625
Philaenus sp.	Gen	*Linaria*	1	0	0.0000	NA	NA
Philaenus sp.	Gen	*Mantisalca*	1	0	0.0000	NA	NA
Philaenus sp.	Gen	*Nigella*	1	0	0.0000	NA	NA
Philaenus sp.	Gen	*Ononis*	3	0	0.0000	0.0000	0.0000
Philaenus sp.	Gen	*Ornithogalum*	1	0	0.0000	NA	NA
Philaenus sp.	Gen	*Papaver*	6	0	0.0000	0.0000	0.0000
Philaenus sp.	Gen	*Pulicaria*	1	0	0.0000	NA	NA
Philaenus sp.	Gen	*Raphanus*	1	0	0.0000	NA	NA
Philaenus sp.	Gen	*Ridolfia*	2	0	0.0000	0.0000	0.0000
Philaenus sp.	Gen	*Scabiosa*	5	1	0.2000	0.4472	0.2000
Philaenus sp.	Gen	*Scolymus*	1	0	0.0000	NA	NA
Philaenus sp.	Gen	*Spergularia*	1	0	0.0000	NA	NA
Philaenus sp.	Gen	*Tolpis*	1	0	0.0000	NA	NA
Philaenus sp.	Gen	*Torilis*	3	0	0.0000	0.0000	0.0000
Philaenus sp.	Gen	*Tribulus*	1	0	0.0000	NA	NA

Table F.1 (cont.) – Summary of abundance of different species of *Xylella fastidiosa* vectors and potential vectors (dependent variable) collected in Alentejo Region during spring of 2017 by 22 environmental factors (independent variable). N = number of samples in each class; Sum = total number of insect vectors; Mean = mean abundance of insect vectors; SD = standard deviation of insect vectors; SE = standard error of the mean. Presence of vectors highlighted in grey

Dependent variable	Independent variable	Class	N	Sum	Mean	SD	SE
Philaenus sp.	Gen	*Urospermum*	1	0	0.0000	NA	NA
Philaenus sp.	Gen	*Verbascum*	5	0	0.0000	0.0000	0.0000
Philaenus sp.	Spe	*Allium ampeloprasum*	1	0	0.0000	NA	NA
Philaenus sp.	Spe	*Ammi majus*	1	0	0.0000	NA	NA
Philaenus sp.	Spe	*Anacyclus radiatus*	8	0	0.0000	0.0000	0.0000
Philaenus sp.	Spe	*Anagallis arvensis*	1	0	0.0000	NA	NA
Philaenus sp.	Spe	*Anchusa azurea*	1	0	0.0000	NA	NA
Philaenus sp.	Spe	*Andryala integrifolia*	10	2	0.2000	0.4216	0.1333
Philaenus sp.	Spe	*Andryala laxiflora*	4	0	0.0000	0.0000	0.0000
Philaenus sp.	Spe	*Cachrys sicula*	4	0	0.0000	0.0000	0.0000
Philaenus sp.	Spe	*Calendula arvensis*	1	0	0.0000	NA	NA
Philaenus sp.	Spe	*Carduus tenuiflorus*	2	0	0.0000	0.0000	0.0000
Philaenus sp.	Spe	*Centaurium pulchellum*	2	0	0.0000	0.0000	0.0000
Philaenus sp.	Spe	*Chamaemelum mixtum*	10	0	0.0000	0.0000	0.0000
Philaenus sp.	Spe	*Chrysanthemum coronarium*	4	0	0.0000	0.0000	0.0000
Philaenus sp.	Spe	*Chrysanthemum segetum*	1	0	0.0000	NA	NA
Philaenus sp.	Spe	*Cichorium intybus*	3	0	0.0000	0.0000	0.0000
Philaenus sp.	Spe	*Cistus crispus*	1	0	0.0000	NA	NA
Philaenus sp.	Spe	*Cistus salvifolius*	2	0	0.0000	0.0000	0.0000
Philaenus sp.	Spe	*Conium maculatum*	1	0	0.0000	NA	NA
Philaenus sp.	Spe	*Convolvulus althaeoides*	2	0	0.0000	0.0000	0.0000
Philaenus sp.	Spe	*Convolvulus arvensis*	9	0	0.0000	0.0000	0.0000
Philaenus sp.	Spe	*Conyza bonariensis*	1	0	0.0000	NA	NA
Philaenus sp.	Spe	*Crepis capillaris*	3	0	0.0000	0.0000	0.0000
Philaenus sp.	Spe	*Crepis sp.*	1	0	0.0000	NA	NA
Philaenus sp.	Spe	*Crepis vesicaria*	1	0	0.0000	NA	NA
Philaenus sp.	Spe	*Daucus carota*	16	2	0.1250	0.3416	0.0854
Philaenus sp.	Spe	*Daucus crinitus*	1	0	0.0000	NA	NA
Philaenus sp.	Spe	*Daucus muricatus*	4	0	0.0000	0.0000	0.0000
Philaenus sp.	Spe	*Echium plantagineum*	15	2	0.1333	0.5164	0.1333
Philaenus sp.	Spe	*Elaeoselinum foetidum*	2	0	0.0000	0.0000	0.0000
Philaenus sp.	Spe	*Erodium moschatum*	1	0	0.0000	NA	NA
Philaenus sp.	Spe	*Foeniculum vulgare*	3	1	0.3333	0.5774	0.3333
Philaenus sp.	Spe	*Galactites tomentosus*	3	2	0.6667	0.5774	0.3333
Philaenus sp.	Spe	*Heliotropium europaeum*	2	0	0.0000	0.0000	0.0000
Philaenus sp.	Spe	*Hirschfeldia incana*	4	0	0.0000	0.0000	0.0000
Philaenus sp.	Spe	*Hypericum perforatum*	2	0	0.0000	0.0000	0.0000
Philaenus sp.	Spe	*Lavatera cretica*	13	1	0.0769	0.2774	0.0769
Philaenus sp.	Spe	*Lavatera trimestris*	3	0	0.0000	0.0000	0.0000
Philaenus sp.	Spe	*Linaria spartea*	1	0	0.0000	NA	NA
Philaenus sp.	Spe	*Mantisalca salmantica*	1	0	0.0000	NA	NA
Philaenus sp.	Spe	*Nigella damascena*	1	0	0.0000	NA	NA
Philaenus sp.	Spe	*Ononis pubescens*	2	0	0.0000	0.0000	0.0000
Philaenus sp.	Spe	*Ononis viscosa*	1	0	0.0000	NA	NA
Philaenus sp.	Spe	*Ornithogalum narbonense*	1	0	0.0000	NA	NA
Philaenus sp.	Spe	*Papaver dubium*	1	0	0.0000	NA	NA
Philaenus sp.	Spe	*Papaver rhoeas*	5	0	0.0000	0.0000	0.0000
Philaenus sp.	Spe	*Pulicaria paludosa*	1	0	0.0000	NA	NA
Philaenus sp.	Spe	*Raphanus raphanistrum*	1	0	0.0000	NA	NA
Philaenus sp.	Spe	*Ridolfia segetum*	2	0	0.0000	0.0000	0.0000
Philaenus sp.	Spe	*Scabiosa atropurpurea*	5	1	0.2000	0.4472	0.2000
Philaenus sp.	Spe	*Scolymus hispanicus*	1	0	0.0000	NA	NA
Philaenus sp.	Spe	*Spergularia purpurea*	1	0	0.0000	NA	NA
Philaenus sp.	Spe	*Tolpis barbata*	1	0	0.0000	NA	NA

Table F.1 (cont.) – Summary of abundance of different species of *Xylella fastidiosa* vectors and potential vectors (dependent variable) collected in Alentejo Region during spring of 2017 by 22 environmental factors (independent variable). N = number of samples in each class; Sum = total number of insect vectors; Mean = mean abundance of insect vectors; SD = standard deviation of insect vectors; SE = standard error of the mean. Presence of vectors highlighted in grey

Dependent variable	Independent variable	Class	N	Sum	Mean	SD	SE
Philaenus sp.	Spe	*Torilis arvensis*	2	0	0.0000	0.0000	0.0000
Philaenus sp.	Spe	*Torilis sp.*	1	0	0.0000	NA	NA
Philaenus sp.	Spe	*Tribulus terrestris*	1	0	0.0000	NA	NA
Philaenus sp.	Spe	*Urospermum picroides*	1	0	0.0000	NA	NA
Philaenus sp.	Spe	*Verbascum sinuatum*	5	0	0.0000	0.0000	0.0000
Philaenus sp.	GU	0	8	1	0.1250	0.3536	0.1250
Philaenus sp.	GU	1	3	0	0.0000	0.0000	0.0000
Philaenus sp.	GU	2	14	0	0.0000	0.0000	0.0000
Philaenus sp.	GU	3	2	0	0.0000	0.0000	0.0000
Philaenus sp.	GU	4	2	1	0.5000	0.7071	0.5000
Philaenus sp.	GU	6	8	4	0.5000	0.7559	0.2673
Philaenus sp.	GU	7	2	1	0.5000	0.7071	0.5000
Philaenus sp.	GU	8	14	0	0.0000	0.0000	0.0000
Philaenus sp.	GU	9	14	3	0.2143	0.8018	0.2143
Philaenus sp.	GU	13	9	0	0.0000	0.0000	0.0000
Philaenus sp.	GU	14	7	0	0.0000	0.0000	0.0000
Philaenus sp.	GU	15	14	3	0.2143	0.8018	0.2143
Philaenus sp.	GU	19	9	0	0.0000	0.0000	0.0000
Philaenus sp.	GU	20	9	0	0.0000	0.0000	0.0000
Philaenus sp.	GU	21	8	0	0.0000	0.0000	0.0000
Philaenus sp.	GU	25	8	0	0.0000	0.0000	0.0000
Philaenus sp.	GU	26	9	0	0.0000	0.0000	0.0000
Philaenus sp.	GU	27	10	0	0.0000	0.0000	0.0000
Philaenus sp.	Host	Mixed ground cover	57	11	0.1930	0.6392	0.0847
Philaenus sp.	Host	Olive	93	2	0.0215	0.1458	0.0151
Philaenus sp.	DistWat	[0, 100]	6	0	0.0000	0.0000	0.0000
Philaenus sp.	DistWat	]100, 500]	26	4	0.1538	0.4641	0.0910
Philaenus sp.	DistWat	]500, 1000]	42	0	0.0000	0.0000	0.0000
Philaenus sp.	DistWat	]1000, 2000]	43	2	0.0465	0.2131	0.0325
Philaenus sp.	DistWat	> 2000	33	7	0.2121	0.7398	0.1288
Philaenus sp.	Alti	[0, 50]	7	1	0.1429	0.3780	0.1429
Philaenus sp.	Alti	]50, 100]	8	2	0.2500	0.7071	0.2500
Philaenus sp.	Alti	]100, 200]	61	2	0.0328	0.1796	0.0230
Philaenus sp.	Alti	]200, 300]	53	5	0.0943	0.4500	0.0618
Philaenus sp.	Alti	> 300	21	3	0.1429	0.6547	0.1429
Philaenus sp.	Asp	Flat	2	0	0.0000	0.0000	0.0000
Philaenus sp.	Asp	North: [0, 45] ∪]316, 360]	48	4	0.0833	0.4535	0.0655
Philaenus sp.	Asp	East:]45, 135]	29	1	0.0345	0.1857	0.0345
Philaenus sp.	Asp	South:]135, 225]	34	6	0.1765	0.5758	0.0987
Philaenus sp.	Asp	West:]225, 315]	37	2	0.0541	0.3288	0.0541
Philaenus sp.	Tmed	19	30	0	0.0000	0.0000	0.0000
Philaenus sp.	Tmed	21	67	6	0.0896	0.5144	0.0628
Philaenus sp.	Tmed	24	14	5	0.3571	0.6333	0.1693
Philaenus sp.	Tmed	26	38	2	0.0526	0.2263	0.0367
Philaenus sp.	Tmed	28	1	0	0.0000	NA	NA
Philaenus sp.	Prec	5	33	5	0.1515	0.4417	0.0769
Philaenus sp.	Prec	10	20	2	0.1000	0.3078	0.0688
Philaenus sp.	Prec	25	38	0	0.0000	0.0000	0.0000
Philaenus sp.	Prec	50	59	6	0.1017	0.5476	0.0713
Philaenus sp.	OlivDist	[0, 50]	62	9	0.1452	0.5072	0.0644
Philaenus sp.	OlivDist	]50, 100]	25	4	0.1600	0.6245	0.1249
Philaenus sp.	OlivDist	]100, 250]	28	0	0.0000	0.0000	0.0000
Philaenus sp.	OlivDist	]250, 1000]	30	0	0.0000	0.0000	0.0000
Philaenus sp.	OlivDist	> 1000	5	0	0.0000	0.0000	0.0000

Table F.1 (cont.) – Summary of abundance of different species of *Xylella fastidiosa* vectors and potential vectors (dependent variable) collected in Alentejo Region during spring of 2017 by 22 environmental factors (independent variable). N = number of samples in each class; Sum = total number of insect vectors; Mean = mean abundance of insect vectors; SD = standard deviation of insect vectors; SE = standard error of the mean. Presence of vectors highlighted in grey

Dependent variable	Independent variable	Class	N	Sum	Mean	SD	SE
Philaenus sp.	Oliv250	0	37	0	0.0000	0.0000	0.0000
Philaenus sp.	Oliv250	]0, 25]	47	4	0.0851	0.3508	0.0512
Philaenus sp.	Oliv250	]25, 50]	29	1	0.0345	0.1857	0.0345
Philaenus sp.	Oliv250	]50, 75]	17	8	0.4706	1.0073	0.2443
Philaenus sp.	Oliv250	]75, 100]	17	0	0.0000	0.0000	0.0000
Philaenus sp.	Oliv250	100	3	0	0.0000	0.0000	0.0000
Philaenus sp.	Oliv500	0	19	0	0.0000	0.0000	0.0000
Philaenus sp.	Oliv500	]0, 25]	68	7	0.1029	0.4617	0.056
Philaenus sp.	Oliv500	]25, 50]	34	6	0.1765	0.5758	0.0987
Philaenus sp.	Oliv500	]50, 75]	22	0	0.0000	0.0000	0.0000
Philaenus sp.	Oliv500	]75, 100]	7	0	0.0000	0.0000	0.0000
Philaenus sp.	Oliv500	100	0	-	-	-	-
Philaenus sp.	Oliv1000	0	9	0	0.0000	0.0000	0.0000
Philaenus sp.	Oliv1000	]0, 25]	83	8	0.0964	0.4310	0.0473
Philaenus sp.	Oliv1000	]25, 50]	40	5	0.1250	0.5158	0.0816
Philaenus sp.	Oliv1000	]50, 75]	17	0	0.0000	0.0000	0.0000
Philaenus sp.	Oliv1000	]75, 100]	1	0	0.0000	NA	NA
Philaenus sp.	Oliv1000	100	0	-	-	-	-
Philaenus sp.	RipDist	[0, 50]	2	0	0.0000	0.0000	0.0000
Philaenus sp.	RipDist	]50, 100]	0	-	-	-	-
Philaenus sp.	RipDist	]100, 250]	1	0	0.0000	NA	NA
Philaenus sp.	RipDist	]250, 1000]	27	3	0.1111	0.4237	0.0815
Philaenus sp.	RipDist	> 1000	120	10	0.0833	0.4217	0.0385
Philaenus sp.	Rip250	0	145	13	0.0897	0.4236	0.0352
Philaenus sp.	Rip250	]0, 25]	5	0	0.0000	0.0000	0.0000
Philaenus sp.	Rip250	]25, 50]	0	-	-	-	-
Philaenus sp.	Rip250	]50, 75]	0	-	-	-	-
Philaenus sp.	Rip250	]75, 100]	0	-	-	-	-
Philaenus sp.	Rip250	100	0	-	-	-	-
Philaenus sp.	Rip500	0	137	10	0.0730	0.3955	0.0338
Philaenus sp.	Rip500	]0, 25]	13	3	0.2308	0.5991	0.1662
Philaenus sp.	Rip500	]25, 50]	0	-	-	-	-
Philaenus sp.	Rip500	]50, 75]	0	-	-	-	-
Philaenus sp.	Rip500	]75, 100]	0	-	-	-	-
Philaenus sp.	Rip500	100	0	-	-	-	-
Philaenus sp.	Rip1000	0	122	10	0.0820	0.4184	0.0379
Philaenus sp.	Rip1000	]0, 25]	28	3	0.1071	0.4163	0.0787
Philaenus sp.	Rip1000	]25, 50]	0	-	-	-	-
Philaenus sp.	Rip1000	]50, 75]	0	-	-	-	-
Philaenus sp.	Rip1000	]75, 100]	0	-	-	-	-
Philaenus sp.	Rip1000	100	0	-	-	-	-
Philaenus sp.	Vine250	0	133	13	0.0977	0.4415	0.0383
Philaenus sp.	Vine250	]0, 25]	13	0	0.0000	0.0000	0.0000
Philaenus sp.	Vine250	]25, 50]	4	0	0.0000	0.0000	0.0000
Philaenus sp.	Vine250	]50, 75]	0	-	-	-	-
Philaenus sp.	Vine250	]75, 100]	0	-	-	-	-
Philaenus sp.	Vine250	100	0	-	-	-	-
Philaenus sp.	Past250	0	70	1	0.0143	0.1195	0.0143
Philaenus sp.	Past250	]0, 25]	58	10	0.1724	0.6251	0.0821
Philaenus sp.	Past250	]25, 50]	16	2	0.1250	0.3416	0.0854
Philaenus sp.	Past250	]50, 75]	6	0	0.0000	0.0000	0.0000
Philaenus sp.	Past250	]75, 100]	0	-	-	-	-
Philaenus sp.	Past250	100	0	-	-	-	-
Philaenus sp.	Holm250	0	114	13	0.1140	0.4752	0.0445

Table F.1 (cont.) – Summary of abundance of different species of *Xylella fastidiosa* vectors and potential vectors (dependent variable) collected in Alentejo Region during spring of 2017 by 22 environmental factors (independent variable). N = number of samples in each class; Sum = total number of insect vectors; Mean = mean abundance of insect vectors; SD = standard deviation of insect vectors; SE = standard error of the mean. Presence of vectors highlighted in grey

Dependent variable	Independent variable	Class	N	Sum	Mean	SD	SE
Philaenus sp.	Holm250	]0, 25]	26	0	0.0000	0.0000	0.0000
Philaenus sp.	Holm250	]25, 50]	2	0	0.0000	0.0000	0.0000
Philaenus sp.	Holm250	]50, 75]	6	0	0.0000	0.0000	0.0000
Philaenus sp.	Holm250	]75, 100]	2	0	0.0000	0.0000	0.0000
Philaenus sp.	Holm250	100	0	-	-	-	-
Philaenus sp.	Cork250	0	122	9	0.0738	0.3674	0.0333
Philaenus sp.	Cork250	]0, 25]	25	4	0.1600	0.6245	0.1249
Philaenus sp.	Cork250	]25, 50]	3	0	0.0000	0.0000	0.0000
Philaenus sp.	Cork250	]50, 75]	0	-	-	-	-
Philaenus sp.	Cork250	]75, 100]	0	-	-	-	-
Philaenus sp.	Cork250	100	0	-	-	-	-
P. spumarius	Fam	Amaryllidaceae	1	0	0.0000	NA	NA
P. spumarius	Fam	Apiaceae	37	1	0.0270	0.1644	0.0270
P. spumarius	Fam	Asparagaceae	1	0	0.0000	NA	NA
P. spumarius	Fam	Asteraceae	57	0	0.0000	0.0000	0.0000
P. spumarius	Fam	Boraginaceae	18	0	0.0000	0.0000	0.0000
P. spumarius	Fam	Brassicaceae	5	0	0.0000	0.0000	0.0000
P. spumarius	Fam	Caryophyllaceae	1	0	0.0000	NA	NA
P. spumarius	Fam	Cistaceae	3	0	0.0000	0.0000	0.0000
P. spumarius	Fam	Convolvulaceae	11	0	0.0000	0.0000	0.0000
P. spumarius	Fam	Dipsacaceae	5	0	0.0000	0.0000	0.0000
P. spumarius	Fam	Fabaceae	3	0	0.0000	0.0000	0.0000
P. spumarius	Fam	Gentiaceae	2	0	0.0000	0.0000	0.0000
P. spumarius	Fam	Geraniaceae	1	0	0.0000	NA	NA
P. spumarius	Fam	Hypericaceae	2	0	0.0000	0.0000	0.0000
P. spumarius	Fam	Malvaceae	16	0	0.0000	0.0000	0.0000
P. spumarius	Fam	Papaveraceae	6	0	0.0000	0.0000	0.0000
P. spumarius	Fam	Plantaginaceae	1	0	0.0000	NA	NA
P. spumarius	Fam	Primulaceae	1	0	0.0000	NA	NA
P. spumarius	Fam	Ranunculaceae	1	0	0.0000	NA	NA
P. spumarius	Fam	Scrophulariaceae	5	0	0.0000	0.0000	0.0000
P. spumarius	Fam	Zygophyllaceae	1	0	0.0000	NA	NA
P. spumarius	Gen	*Allium*	1	0	0.0000	NA	NA
P. spumarius	Gen	*Ammi*	1	0	0.0000	NA	NA
P. spumarius	Gen	*Anacyclus*	8	0	0.0000	0.0000	0.0000
P. spumarius	Gen	*Anagallis*	1	0	0.0000	NA	NA
P. spumarius	Gen	*Anchusa*	1	0	0.0000	NA	NA
P. spumarius	Gen	*Andryala*	14	0	0.0000	0.0000	0.0000
P. spumarius	Gen	*Cachrys*	4	0	0.0000	0.0000	0.0000
P. spumarius	Gen	*Calendula*	1	0	0.0000	NA	NA
P. spumarius	Gen	*Carduus*	2	0	0.0000	0.0000	0.0000
P. spumarius	Gen	*Centaurium*	2	0	0.0000	0.0000	0.0000
P. spumarius	Gen	*Chamaemelum*	10	0	0.0000	0.0000	0.0000
P. spumarius	Gen	*Chrysanthemum*	5	0	0.0000	0.0000	0.0000
P. spumarius	Gen	*Cichorium*	3	0	0.0000	0.0000	0.0000
P. spumarius	Gen	*Cistus*	3	0	0.0000	0.0000	0.0000
P. spumarius	Gen	*Conium*	1	0	0.0000	NA	NA
P. spumarius	Gen	*Convolvulus*	11	0	0.0000	0.0000	0.0000
P. spumarius	Gen	*Conyza*	1	0	0.0000	NA	NA
P. spumarius	Gen	*Crepis*	5	0	0.0000	0.0000	0.0000
P. spumarius	Gen	*Daucus*	21	1	0.0476	0.2182	0.0476
P. spumarius	Gen	*Echium*	15	0	0.0000	0.0000	0.0000
P. spumarius	Gen	*Elaeoselinum*	2	0	0.0000	0.0000	0.0000
P. spumarius	Gen	*Erodium*	1	0	0.0000	NA	NA

Table F.1 (cont.) – Summary of abundance of different species of *Xylella fastidiosa* vectors and potential vectors (dependent variable) collected in Alentejo Region during spring of 2017 by 22 environmental factors (independent variable). N = number of samples in each class; Sum = total number of insect vectors; Mean = mean abundance of insect vectors; SD = standard deviation of insect vectors; SE = standard error of the mean. Presence of vectors highlighted in grey

Dependent variable	Independent variable	Class	N	Sum	Mean	SD	SE
P. spumarius	Gen	*Foeniculum*	3	0	0.0000	0.0000	0.0000
P. spumarius	Gen	*Galactites*	3	0	0.0000	0.0000	0.0000
P. spumarius	Gen	*Heliotropium*	2	0	0.0000	0.0000	0.0000
P. spumarius	Gen	*Hirschfeldia*	4	0	0.0000	0.0000	0.0000
P. spumarius	Gen	*Hypericum*	2	0	0.0000	0.0000	0.0000
P. spumarius	Gen	*Lavatera*	16	0	0.0000	0.0000	0.0000
P. spumarius	Gen	*Linaria*	1	0	0.0000	NA	NA
P. spumarius	Gen	*Mantisalca*	1	0	0.0000	NA	NA
P. spumarius	Gen	*Nigella*	1	0	0.0000	NA	NA
P. spumarius	Gen	*Ononis*	3	0	0.0000	0.0000	0.0000
P. spumarius	Gen	*Ornithogalum*	1	0	0.0000	NA	NA
P. spumarius	Gen	*Papaver*	6	0	0.0000	0.0000	0.0000
P. spumarius	Gen	*Pulicaria*	1	0	0.0000	NA	NA
P. spumarius	Gen	*Raphanus*	1	0	0.0000	NA	NA
P. spumarius	Gen	*Ridolfia*	2	0	0.0000	0.0000	0.0000
P. spumarius	Gen	*Scabiosa*	5	0	0.0000	0.0000	0.0000
P. spumarius	Gen	*Scolymus*	1	0	0.0000	NA	NA
P. spumarius	Gen	*Spergularia*	1	0	0.0000	NA	NA
P. spumarius	Gen	*Tolpis*	1	0	0.0000	NA	NA
P. spumarius	Gen	*Torilis*	3	0	0.0000	0.0000	0.0000
P. spumarius	Gen	*Tribulus*	1	0	0.0000	NA	NA
P. spumarius	Gen	*Urospermum*	1	0	0.0000	NA	NA
P. spumarius	Gen	*Verbascum*	5	0	0.0000	0.0000	0.0000
P. spumarius	Spe	*Allium ampeloprasum*	1	0	0.0000	NA	NA
P. spumarius	Spe	*Ammi majus*	1	0	0.0000	NA	NA
P. spumarius	Spe	*Anacyclus radiatus*	8	0	0.0000	0.0000	0.0000
P. spumarius	Spe	*Anagallis arvensis*	1	0	0.0000	NA	NA
P. spumarius	Spe	*Anchusa azurea*	1	0	0.0000	NA	NA
P. spumarius	Spe	*Andryala integrifolia*	10	0	0.0000	0.0000	0.0000
P. spumarius	Spe	*Andryala laxiflora*	4	0	0.0000	0.0000	0.0000
P. spumarius	Spe	*Cachrys sicula*	4	0	0.0000	0.0000	0.0000
P. spumarius	Spe	*Calendula arvensis*	1	0	0.0000	NA	NA
P. spumarius	Spe	*Carduus tenuiflorus*	2	0	0.0000	0.0000	0.0000
P. spumarius	Spe	*Centaurium pulchellum*	2	0	0.0000	0.0000	0.0000
P. spumarius	Spe	*Chamaemelum mixtum*	10	0	0.0000	0.0000	0.0000
P. spumarius	Spe	*Chrysanthemum coronarium*	4	0	0.0000	0.0000	0.0000
P. spumarius	Spe	*Chrysanthemum segetum*	1	0	0.0000	NA	NA
P. spumarius	Spe	*Cichorium intybus*	3	0	0.0000	0.0000	0.0000
P. spumarius	Spe	*Cistus crispus*	1	0	0.0000	NA	NA
P. spumarius	Spe	*Cistus salvifolius*	2	0	0.0000	0.0000	0.0000
P. spumarius	Spe	*Conium maculatum*	1	0	0.0000	NA	NA
P. spumarius	Spe	*Convolvulus althaeoides*	2	0	0.0000	0.0000	0.0000
P. spumarius	Spe	*Convolvulus arvensis*	9	0	0.0000	0.0000	0.0000
P. spumarius	Spe	*Conyza bonariensis*	1	0	0.0000	NA	NA
P. spumarius	Spe	*Crepis capillaris*	3	0	0.0000	0.0000	0.0000
P. spumarius	Spe	*Crepis sp.*	1	0	0.0000	NA	NA
P. spumarius	Spe	*Crepis vesicaria*	1	0	0.0000	NA	NA
P. spumarius	Spe	*Daucus carota*	16	1	0.0625	0.2500	0.0625
P. spumarius	Spe	*Daucus crinitus*	1	0	0.0000	NA	NA
P. spumarius	Spe	*Daucus muricatus*	4	0	0.0000	0.0000	0.0000
P. spumarius	Spe	*Echium plantagineum*	15	0	0.0000	0.0000	0.0000
P. spumarius	Spe	*Elaeoselinum foetidum*	2	0	0.0000	0.0000	0.0000
P. spumarius	Spe	*Erodium moschatum*	1	0	0.0000	NA	NA
P. spumarius	Spe	*Foeniculum vulgare*	3	0	0.0000	0.0000	0.0000

Table F.1 (cont.) – Summary of abundance of different species of *Xylella fastidiosa* vectors and potential vectors (dependent variable) collected in Alentejo Region during spring of 2017 by 22 environmental factors (independent variable). N = number of samples in each class; Sum = total number of insect vectors; Mean = mean abundance of insect vectors; SD = standard deviation of insect vectors; SE = standard error of the mean. Presence of vectors highlighted in grey

Dependent variable	Independent variable	Class	N	Sum	Mean	SD	SE
P. spumarius	Spe	*Galactites tomentosus*	3	0	0.0000	0.0000	0.0000
P. spumarius	Spe	*Heliotropium europaeum*	2	0	0.0000	0.0000	0.0000
P. spumarius	Spe	*Hirschfeldia incana*	4	0	0.0000	0.0000	0.0000
P. spumarius	Spe	*Hypericum perforatum*	2	0	0.0000	0.0000	0.0000
P. spumarius	Spe	*Lavatera cretica*	13	0	0.0000	0.0000	0.0000
P. spumarius	Spe	*Lavatera trimestris*	3	0	0.0000	0.0000	0.0000
P. spumarius	Spe	*Linaria spartea*	1	0	0.0000	NA	NA
P. spumarius	Spe	*Mantisalca salmantica*	1	0	0.0000	NA	NA
P. spumarius	Spe	*Nigella damascena*	1	0	0.0000	NA	NA
P. spumarius	Spe	*Ononis pubescens*	2	0	0.0000	0.0000	0.0000
P. spumarius	Spe	*Ononis viscosa*	1	0	0.0000	NA	NA
P. spumarius	Spe	*Ornithogalum narbonense*	1	0	0.0000	NA	NA
P. spumarius	Spe	*Papaver dubium*	1	0	0.0000	NA	NA
P. spumarius	Spe	*Papaver rhoeas*	5	0	0.0000	0.0000	0.0000
P. spumarius	Spe	*Pulicaria paludosa*	1	0	0.0000	NA	NA
P. spumarius	Spe	*Raphanus raphanistrum*	1	0	0.0000	NA	NA
P. spumarius	Spe	*Ridolfia segetum*	2	0	0.0000	0.0000	0.0000
P. spumarius	Spe	*Scabiosa atropurpurea*	5	0	0.0000	0.0000	0.0000
P. spumarius	Spe	*Scolymus hispanicus*	1	0	0.0000	NA	NA
P. spumarius	Spe	*Spergularia purpurea*	1	0	0.0000	NA	NA
P. spumarius	Spe	*Tolpis barbata*	1	0	0.0000	NA	NA
P. spumarius	Spe	*Torilis arvensis*	2	0	0.0000	0.0000	0.0000
P. spumarius	Spe	*Torilis sp.*	1	0	0.0000	NA	NA
P. spumarius	Spe	*Tribulus terrestris*	1	0	0.0000	NA	NA
P. spumarius	Spe	*Urospermum picroides*	1	0	0.0000	NA	NA
P. spumarius	Spe	*Verbascum sinuatum*	5	0	0.0000	0.0000	0.0000
P. spumarius	GU	0	8	1	0.1250	0.3536	0.1250
P. spumarius	GU	1	3	0	0.0000	0.0000	0.0000
P. spumarius	GU	2	14	0	0.0000	0.0000	0.0000
P. spumarius	GU	3	2	0	0.0000	0.0000	0.0000
P. spumarius	GU	4	2	0	0.0000	0.0000	0.0000
P. spumarius	GU	6	8	0	0.0000	0.0000	0.0000
P. spumarius	GU	7	2	0	0.0000	0.0000	0.0000
P. spumarius	GU	8	14	0	0.0000	0.0000	0.0000
P. spumarius	GU	9	14	0	0.0000	0.0000	0.0000
P. spumarius	GU	13	9	0	0.0000	0.0000	0.0000
P. spumarius	GU	14	7	0	0.0000	0.0000	0.0000
P. spumarius	GU	15	14	0	0.0000	0.0000	0.0000
P. spumarius	GU	19	9	0	0.0000	0.0000	0.0000
P. spumarius	GU	20	9	0	0.0000	0.0000	0.0000
P. spumarius	GU	21	8	0	0.0000	0.0000	0.0000
P. spumarius	GU	25	8	0	0.0000	0.0000	0.0000
P. spumarius	GU	26	9	0	0.0000	0.0000	0.0000
P. spumarius	GU	27	10	0	0.0000	0.0000	0.0000
P. spumarius	Host	Mixed ground cover	57	1	0.0175	0.1325	0.0175
P. spumarius	Host	Olive	93	0	0.0000	0.0000	0.0000
P. spumarius	DistWat	[0, 100]	6	0	0.0000	0.0000	0.0000
P. spumarius	DistWat	]100, 500]	26	1	0.0385	0.1961	0.0385
P. spumarius	DistWat	]500, 1000]	42	0	0.0000	0.0000	0.0000
P. spumarius	DistWat	]1000, 2000]	43	0	0.0000	0.0000	0.0000
P. spumarius	DistWat	> 2000	33	0	0.0000	0.0000	0.0000
P. spumarius	Alti	[0, 50]	7	1	0.1429	0.3780	0.1429
P. spumarius	Alti	]50, 100]	8	0	0.0000	0.0000	0.0000
P. spumarius	Alti	]100, 200]	61	0	0.0000	0.0000	0.0000

Table F.1 (cont.) – Summary of abundance of different species of *Xylella fastidiosa* vectors and potential vectors (dependent variable) collected in Alentejo Region during spring of 2017 by 22 environmental factors (independent variable). N = number of samples in each class; Sum = total number of insect vectors; Mean = mean abundance of insect vectors; SD = standard deviation of insect vectors; SE = standard error of the mean. Presence of vectors highlighted in grey

Dependent variable	Independent variable	Class	N	Sum	Mean	SD	SE
P. spumarius	Alti	]200, 300]	53	0	0.0000	0.0000	0.0000
P. spumarius	Alti	> 300	21	0	0.0000	0.0000	0.0000
P. spumarius	Asp	Flat	2	0	0.0000	0.0000	0.0000
P. spumarius	Asp	North: [0, 45] ∪]316, 360]	48	1	0.0208	0.1443	0.0208
P. spumarius	Asp	East:]45, 135]	29	0	0.0000	0.0000	0.0000
P. spumarius	Asp	South:]135, 225]	34	0	0.0000	0.0000	0.0000
P. spumarius	Asp	West:]225, 315]	37	0	0.0000	0.0000	0.0000
P. spumarius	Tmed	19	30	0	0.0000	0.0000	0.0000
P. spumarius	Tmed	21	67	0	0.0000	0.0000	0.0000
P. spumarius	Tmed	24	14	1	0.0714	0.2673	0.0714
P. spumarius	Tmed	26	38	0	0.0000	0.0000	0.0000
P. spumarius	Tmed	28	1	0	0.0000	NA	NA
P. spumarius	Prec	5	33	1	0.0303	0.1741	0.0303
P. spumarius	Prec	10	20	0	0.0000	0.0000	0.0000
P. spumarius	Prec	25	38	0	0.0000	0.0000	0.0000
P. spumarius	Prec	50	59	0	0.0000	0.0000	0.0000
P. spumarius	OlivDist	[0, 50]	62	1	0.0161	0.1270	0.0161
P. spumarius	OlivDist	]50, 100]	25	0	0.0000	0.0000	0.0000
P. spumarius	OlivDist	]100, 250]	28	0	0.0000	0.0000	0.0000
P. spumarius	OlivDist	]250, 1000]	30	0	0.0000	0.0000	0.0000
P. spumarius	OlivDist	> 1000	5	0	0.0000	0.0000	0.0000
P. spumarius	Oliv250	0	37	0	0.0000	0.0000	0.0000
P. spumarius	Oliv250	]0, 25]	47	1	0.0213	0.1459	0.0213
P. spumarius	Oliv250	]25, 50]	29	0	0.0000	0.0000	0.0000
P. spumarius	Oliv250	]50, 75]	17	0	0.0000	0.0000	0.0000
P. spumarius	Oliv250	]75, 100]	17	0	0.0000	0.0000	0.0000
P. spumarius	Oliv250	100	3	0	0.0000	0.0000	0.0000
P. spumarius	Oliv500	0	19	0	0.0000	0.0000	0.0000
P. spumarius	Oliv500	]0, 25]	68	1	0.0147	0.1213	0.0147
P. spumarius	Oliv500	]25, 50]	34	0	0.0000	0.0000	0.0000
P. spumarius	Oliv500	]50, 75]	22	0	0.0000	0.0000	0.0000
P. spumarius	Oliv500	]75, 100]	7	0	0.0000	0.0000	0.0000
P. spumarius	Oliv500	100	0	-	-	-	-
P. spumarius	Oliv1000	0	9	0	0.0000	0.0000	0.0000
P. spumarius	Oliv1000	]0, 25]	83	1	0.0120	0.1098	0.0120
P. spumarius	Oliv1000	]25, 50]	40	0	0.0000	0.0000	0.0000
P. spumarius	Oliv1000	]50, 75]	17	0	0.0000	0.0000	0.0000
P. spumarius	Oliv1000	]75, 100]	1	0	0.0000	NA	NA
P. spumarius	Oliv1000	100	0	-	-	-	-
P. spumarius	RipDist	[0, 50]	2	0	0.0000	0.0000	0.0000
P. spumarius	RipDist	]50, 100]	0	-	-	-	-
P. spumarius	RipDist	]100, 250]	1	0	0.0000	NA	NA
P. spumarius	RipDist	]250, 1000]	27	0	0.0000	0.0000	0.0000
P. spumarius	RipDist	> 1000	120	1	0.0083	0.0913	0.0083
P. spumarius	Rip250	0	145	1	0.0069	0.0830	0.0069
P. spumarius	Rip250	]0, 25]	5	0	0.0000	0.0000	0.0000
P. spumarius	Rip250	]25, 50]	0	-	-	-	-
P. spumarius	Rip250	]50, 75]	0	-	-	-	-
P. spumarius	Rip250	]75, 100]	0	-	-	-	-
P. spumarius	Rip250	100	0	-	-	-	-
P. spumarius	Rip500	0	137	1	0.0073	0.0854	0.0073
P. spumarius	Rip500	]0, 25]	13	0	0.0000	0.0000	0.0000
P. spumarius	Rip500	]25, 50]	0	-	-	-	-
P. spumarius	Rip500	]50, 75]	0	-	-	-	-

Table F.1 (cont.) – Summary of abundance of different species of *Xylella fastidiosa* vectors and potential vectors (dependent variable) collected in Alentejo Region during spring of 2017 by 22 environmental factors (independent variable). N = number of samples in each class; Sum = total number of insect vectors; Mean = mean abundance of insect vectors; SD = standard deviation of insect vectors; SE = standard error of the mean. Presence of vectors highlighted in grey

Dependent variable	Independent variable	Class	N	Sum	Mean	SD	SE
P. spumarius	Rip500	]75, 100]	0	-	-	-	-
P. spumarius	Rip500	100	0	-	-	-	-
P. spumarius	Rip1000	0	122	1	0.0082	0.0905	0.0082
P. spumarius	Rip1000	]0, 25]	28	0	0.0000	0.0000	0.0000
P. spumarius	Rip1000	]25, 50]	0	-	-	-	-
P. spumarius	Rip1000	]50, 75]	0	-	-	-	-
P. spumarius	Rip1000	]75, 100]	0	-	-	-	-
P. spumarius	Rip1000	100	0	-	-	-	-
P. spumarius	Vine250	0	133	1	0.0075	0.0867	0.0075
P. spumarius	Vine250	]0, 25]	13	0	0.0000	0.0000	0.0000
P. spumarius	Vine250	]25, 50]	4	0	0.0000	0.0000	0.0000
P. spumarius	Vine250	]50, 75]	0	-	-	-	-
P. spumarius	Vine250	]75, 100]	0	-	-	-	-
P. spumarius	Vine250	100	0	-	-	-	-
P. spumarius	Past250	0	70	1	0.0143	0.1195	0.0143
P. spumarius	Past250	]0, 25]	58	0	0.0000	0.0000	0.0000
P. spumarius	Past250	]25, 50]	16	0	0.0000	0.0000	0.0000
P. spumarius	Past250	]50, 75]	6	0	0.0000	0.0000	0.0000
P. spumarius	Past250	]75, 100]	0	-	-	-	-
P. spumarius	Past250	100	0	-	-	-	-
P. spumarius	Holm250	0	114	1	0.0088	0.0937	0.0088
P. spumarius	Holm250	]0, 25]	26	0	0.0000	0.0000	0.0000
P. spumarius	Holm250	]25, 50]	2	0	0.0000	0.0000	0.0000
P. spumarius	Holm250	]50, 75]	6	0	0.0000	0.0000	0.0000
P. spumarius	Holm250	]75, 100]	2	0	0.0000	0.0000	0.0000
P. spumarius	Holm250	100	0	-	-	-	-
P. spumarius	Cork250	0	122	0	0.0000	0.0000	0.0000
P. spumarius	Cork250	]0, 25]	25	1	0.0400	0.2000	0.0400
P. spumarius	Cork250	]25, 50]	3	0	0.0000	0.0000	0.0000
P. spumarius	Cork250	]50, 75]	0	-	-	-	-
P. spumarius	Cork250	]75, 100]	0	-	-	-	-
P. spumarius	Cork250	100	0	-	-	-	-
P. tesselatus	Fam	Amaryllidaceae	1	0	0.0000	NA	NA
P. tesselatus	Fam	Apiaceae	37	6	0.1622	0.5008	0.0823
P. tesselatus	Fam	Asparagaceae	1	0	0.0000	NA	NA
P. tesselatus	Fam	Asteraceae	57	8	0.1404	0.4795	0.0635
P. tesselatus	Fam	Boraginaceae	18	2	0.1111	0.3234	0.0762
P. tesselatus	Fam	Brassicaceae	5	0	0.0000	0.0000	0.0000
P. tesselatus	Fam	Caryophyllaceae	1	0	0.0000	NA	NA
P. tesselatus	Fam	Cistaceae	3	0	0.0000	0.0000	0.0000
P. tesselatus	Fam	Convolvulaceae	11	1	0.0909	0.3015	0.0909
P. tesselatus	Fam	Dipsacaceae	5	1	0.2000	0.4472	0.2000
P. tesselatus	Fam	Fabaceae	3	0	0.0000	0.0000	0.0000
P. tesselatus	Fam	Gentiaceae	2	0	0.0000	0.0000	0.0000
P. tesselatus	Fam	Geraniaceae	1	0	0.0000	NA	NA
P. tesselatus	Fam	Hypericaceae	2	0	0.0000	0.0000	0.0000
P. tesselatus	Fam	Malvaceae	16	3	0.1875	0.5439	0.1360
P. tesselatus	Fam	Papaveraceae	6	0	0.0000	0.0000	0.0000
P. tesselatus	Fam	Plantaginaceae	1	0	0.0000	NA	NA
P. tesselatus	Fam	Primulaceae	1	0	0.0000	NA	NA
P. tesselatus	Fam	Ranunculaceae	1	0	0.0000	NA	NA
P. tesselatus	Fam	Scrophulariaceae	5	0	0.0000	0.0000	0.0000
P. tesselatus	Fam	Zygophyllaceae	1	0	0.0000	NA	NA
P. tesselatus	Gen	*Allium*	1	0	0.0000	NA	NA

Table F.1 (cont.) – Summary of abundance of different species of *Xylella fastidiosa* vectors and potential vectors (dependent variable) collected in Alentejo Region during spring of 2017 by 22 environmental factors (independent variable). N = number of samples in each class; Sum = total number of insect vectors; Mean = mean abundance of insect vectors; SD = standard deviation of insect vectors; SE = standard error of the mean. Presence of vectors highlighted in grey

Dependent variable	Independent variable	Class	N	Sum	Mean	SD	SE
P. tesselatus	Gen	*Ammi*	1	0	0.0000	NA	NA
P. tesselatus	Gen	*Anacyclus*	8	0	0.0000	0.0000	0.0000
P. tesselatus	Gen	*Anagallis*	1	0	0.0000	NA	NA
P. tesselatus	Gen	*Anchusa*	1	0	0.0000	NA	NA
P. tesselatus	Gen	*Andryala*	14	1	0.0714	0.2673	0.0714
P. tesselatus	Gen	*Cachrys*	4	0	0.0000	0.0000	0.0000
P. tesselatus	Gen	*Calendula*	1	0	0.0000	NA	NA
P. tesselatus	Gen	*Carduus*	2	0	0.0000	0.0000	0.0000
P. tesselatus	Gen	*Centaurium*	2	0	0.0000	0.0000	0.0000
P. tesselatus	Gen	*Chamaemelum*	10	4	0.4000	0.8433	0.2667
P. tesselatus	Gen	*Chrysanthemum*	5	0	0.0000	0.0000	0.0000
P. tesselatus	Gen	*Cichorium*	3	0	0.0000	0.0000	0.0000
P. tesselatus	Gen	*Cistus*	3	0	0.0000	0.0000	0.0000
P. tesselatus	Gen	*Conium*	1	1	1	NA	NA
P. tesselatus	Gen	*Convolvulus*	11	1	0.0909	0.3015	0.0909
P. tesselatus	Gen	*Conyza*	1	0	0.0000	NA	NA
P. tesselatus	Gen	*Crepis*	5	1	0.2000	0.4472	0.2000
P. tesselatus	Gen	*Daucus*	21	0	0.0000	0.0000	0.0000
P. tesselatus	Gen	*Echium*	15	2	0.1333	0.3519	0.0909
P. tesselatus	Gen	*Elaeoselinum*	2	2	1	1,4142	1
P. tesselatus	Gen	*Erodium*	1	0	0.0000	NA	NA
P. tesselatus	Gen	*Foeniculum*	3	0	0.0000	0.0000	0.0000
P. tesselatus	Gen	*Galactites*	3	2	0.6667	1.1547	0.6667
P. tesselatus	Gen	*Heliotropium*	2	0	0.0000	0.0000	0.0000
P. tesselatus	Gen	*Hirschfeldia*	4	0	0.0000	0.0000	0.0000
P. tesselatus	Gen	*Hypericum*	2	0	0.0000	0.0000	0.0000
P. tesselatus	Gen	*Lavatera*	16	3	0.1875	0.5439	0.1360
P. tesselatus	Gen	*Linaria*	1	0	0.0000	NA	NA
P. tesselatus	Gen	*Mantisalca*	1	0	0.0000	NA	NA
P. tesselatus	Gen	*Nigella*	1	0	0.0000	NA	NA
P. tesselatus	Gen	*Ononis*	3	0	0.0000	0.0000	0.0000
P. tesselatus	Gen	*Ornithogalum*	1	0	0.0000	NA	NA
P. tesselatus	Gen	*Papaver*	6	0	0.0000	0.0000	0.0000
P. tesselatus	Gen	*Pulicaria*	1	0	0.0000	NA	NA
P. tesselatus	Gen	*Raphanus*	1	0	0.0000	NA	NA
P. tesselatus	Gen	*Ridolfia*	2	2	1	1,4142	1
P. tesselatus	Gen	*Scabiosa*	5	1	0.2000	0.4472	0.2000
P. tesselatus	Gen	*Scolymus*	1	0	0.0000	NA	NA
P. tesselatus	Gen	*Spergularia*	1	0	0.0000	NA	NA
P. tesselatus	Gen	*Tolpis*	1	0	0.0000	NA	NA
P. tesselatus	Gen	*Torilis*	3	1	0.3333	0.5774	0.3333
P. tesselatus	Gen	*Tribulus*	1	0	0.0000	NA	NA
P. tesselatus	Gen	*Urospermum*	1	0	0.0000	NA	NA
P. tesselatus	Gen	*Verbascum*	5	0	0.0000	0.0000	0.0000
P. tesselatus	Spe	*Allium ampeloprasum*	1	0	0.0000	NA	NA
P. tesselatus	Spe	*Ammi majus*	1	0	0.0000	NA	NA
P. tesselatus	Spe	*Anacyclus radiatus*	8	0	0.0000	0.0000	0.0000
P. tesselatus	Spe	*Anagallis arvensis*	1	0	0.0000	NA	NA
P. tesselatus	Spe	*Anchusa azurea*	1	0	0.0000	NA	NA
P. tesselatus	Spe	*Andryala integrifolia*	10	1	0.1000	0.3162	0.1000
P. tesselatus	Spe	*Andryala laxiflora*	4	0	0.0000	0.0000	0.0000
P. tesselatus	Spe	*Cachrys sicula*	4	0	0.0000	0.0000	0.0000
P. tesselatus	Spe	*Calendula arvensis*	1	0	0.0000	NA	NA
P. tesselatus	Spe	*Carduus tenuiflorus*	2	0	0.0000	0.0000	0.0000

Table F.1 (cont.) – Summary of abundance of different species of *Xylella fastidiosa* vectors and potential vectors (dependent variable) collected in Alentejo Region during spring of 2017 by 22 environmental factors (independent variable). N = number of samples in each class; Sum = total number of insect vectors; Mean = mean abundance of insect vectors; SD = standard deviation of insect vectors; SE = standard error of the mean. Presence of vectors highlighted in grey

Dependent variable	Independent variable	Class	N	Sum	Mean	SD	SE
P. tesselatus	Spe	*Centaurium pulchellum*	2	0	0.0000	0.0000	0.0000
P. tesselatus	Spe	*Chamaemelum mixtum*	10	4	0.4000	0.8433	0.2667
P. tesselatus	Spe	*Chrysanthemum coronarium*	4	0	0.0000	0.0000	0.0000
P. tesselatus	Spe	*Chrysanthemum segetum*	1	0	0.0000	NA	NA
P. tesselatus	Spe	*Cichorium intybus*	3	0	0.0000	0.0000	0.0000
P. tesselatus	Spe	*Cistus crispus*	1	0	0.0000	NA	NA
P. tesselatus	Spe	*Cistus salvifolius*	2	0	0.0000	0.0000	0.0000
P. tesselatus	Spe	*Conium maculatum*	1	1	1	NA	NA
P. tesselatus	Spe	*Convolvulus althaeoides*	2	0	0.0000	0.0000	0.0000
P. tesselatus	Spe	*Convolvulus arvensis*	9	1	0.1111	0.3333	0.1111
P. tesselatus	Spe	*Conyza bonariensis*	1	0	0.0000	NA	NA
P. tesselatus	Spe	*Crepis capillaris*	3	1	0.3333	0.5774	0.3333
P. tesselatus	Spe	*Crepis sp.*	1	0	0.0000	NA	NA
P. tesselatus	Spe	*Crepis vesicaria*	1	0	0.0000	NA	NA
P. tesselatus	Spe	*Daucus carota*	16	0	0.0000	0.0000	0.0000
P. tesselatus	Spe	*Daucus crinitus*	1	0	0.0000	NA	NA
P. tesselatus	Spe	*Daucus muricatus*	4	0	0.0000	0.0000	0.0000
P. tesselatus	Spe	*Echium plantagineum*	15	2	0.1333	0.3519	0.0909
P. tesselatus	Spe	*Elaeoselinum foetidum*	2	2	1	1,4142	1
P. tesselatus	Spe	*Erodium moschatum*	1	0	0.0000	NA	NA
P. tesselatus	Spe	*Foeniculum vulgare*	3	0	0.0000	0.0000	0.0000
P. tesselatus	Spe	*Galactites tomentosus*	3	2	0.6667	1.1547	0.6667
P. tesselatus	Spe	*Heliotropium europaeum*	2	0	0.0000	0.0000	0.0000
P. tesselatus	Spe	*Hirschfeldia incana*	4	0	0.0000	0.0000	0.0000
P. tesselatus	Spe	*Hypericum perforatum*	2	0	0.0000	0.0000	0.0000
P. tesselatus	Spe	*Lavatera cretica*	13	2	0.1538	0.5547	0.1538
P. tesselatus	Spe	*Lavatera trimestris*	3	1	0.3333	0.5774	0.3333
P. tesselatus	Spe	*Linaria spartea*	1	0	0.0000	NA	NA
P. tesselatus	Spe	*Mantisalca salmantica*	1	0	0.0000	NA	NA
P. tesselatus	Spe	*Nigella damascena*	1	0	0.0000	NA	NA
P. tesselatus	Spe	*Ononis pubescens*	2	0	0.0000	0.0000	0.0000
P. tesselatus	Spe	*Ononis viscosa*	1	0	0.0000	NA	NA
P. tesselatus	Spe	*Ornithogalum narbonense*	1	0	0.0000	NA	NA
P. tesselatus	Spe	*Papaver dubium*	1	0	0.0000	NA	NA
P. tesselatus	Spe	*Papaver rhoeas*	5	0	0.0000	0.0000	0.0000
P. tesselatus	Spe	*Pulicaria paludosa*	1	0	0.0000	NA	NA
P. tesselatus	Spe	*Raphanus raphanistrum*	1	0	0.0000	NA	NA
P. tesselatus	Spe	*Ridolfia segetum*	2	2	1	1,4142	1
P. tesselatus	Spe	*Scabiosa atropurpurea*	5	1	0.2000	0.4472	0.2000
P. tesselatus	Spe	*Scolymus hispanicus*	1	0	0.0000	NA	NA
P. tesselatus	Spe	*Spergularia purpurea*	1	0	0.0000	NA	NA
P. tesselatus	Spe	*Tolpis barbata*	1	0	0.0000	NA	NA
P. tesselatus	Spe	*Torilis arvensis*	2	0	0.0000	0.0000	0.0000
P. tesselatus	Spe	*Torilis sp.*	1	1	1	NA	NA
P. tesselatus	Spe	*Tribulus terrestris*	1	0	0.0000	NA	NA
P. tesselatus	Spe	*Urospermum picroides*	1	0	0.0000	NA	NA
P. tesselatus	Spe	*Verbascum sinuatum*	5	0	0.0000	0.0000	0.0000
P. tesselatus	GU	0	8	0	0.0000	0.0000	0.0000
P. tesselatus	GU	1	3	0	0.0000	0.0000	0.0000
P. tesselatus	GU	2	14	1	0.0714	0.2673	0.0191
P. tesselatus	GU	3	2	1	0.5000	0.7071	0.3536
P. tesselatus	GU	4	2	0	0.0000	0.0000	0.0000
P. tesselatus	GU	6	8	3	0.3750	1.0607	0.1326
P. tesselatus	GU	7	2	1	0.5000	0.7071	0.3536

Table F.1 (cont.) – Summary of abundance of different species of *Xylella fastidiosa* vectors and potential vectors (dependent variable) collected in Alentejo Region during spring of 2017 by 22 environmental factors (independent variable). N = number of samples in each class; Sum = total number of insect vectors; Mean = mean abundance of insect vectors; SD = standard deviation of insect vectors; SE = standard error of the mean. Presence of vectors highlighted in grey

Dependent variable	Independent variable	Class	N	Sum	Mean	SD	SE
P. tesselatus	GU	8	14	11	0.7857	0.9750	0.2100
P. tesselatus	GU	9	14	4	0.2857	0.4688	0.0764
P. tesselatus	GU	13	9	6	0.6667	0.8660	0.2222
P. tesselatus	GU	14	7	6	0.8571	0.8997	0.3240
P. tesselatus	GU	15	14	5	0.3571	1.0818	0.0955
P. tesselatus	GU	19	9	4	0.4444	0.8819	0.1481
P. tesselatus	GU	20	9	2	0.2222	0.4410	0.0741
P. tesselatus	GU	21	8	5	0.6250	0.7440	0.2210
P. tesselatus	GU	25	8	0	0.0000	0.0000	0.0000
P. tesselatus	GU	26	9	1	0.1111	0.3333	0.0370
P. tesselatus	GU	27	10	7	0.7000	1.6364	0.2214
P. tesselatus	Host	Mixed ground cover	57	30	0.5263	1.0708	0.0697
P. tesselatus	Host	Olive	93	27	0.2903	0.6004	0.0301
P. tesselatus	DistWat	[0, 100]	6	1	0.1667	0.4082	0.0680
P. tesselatus	DistWat	]100, 500]	26	4	0.1538	0.4641	0.0302
P. tesselatus	DistWat	]500, 1000]	42	14	0.3333	0.7213	0.0514
P. tesselatus	DistWat	]1000, 2000]	43	23	0.5349	1.0316	0.0816
P. tesselatus	DistWat	> 2000	33	15	0.4545	0.8693	0.0791
P. tesselatus	Alti	[0, 50]	7	0	0.0000	0.0000	0.0000
P. tesselatus	Alti	]50, 100]	8	2	0.2500	0.7071	0.0884
P. tesselatus	Alti	]100, 200]	61	19	0.3115	0.7425	0.0399
P. tesselatus	Alti	]200, 300]	53	28	0.5283	1.0115	0.0726
P. tesselatus	Alti	> 300	21	8	0.3810	0.5896	0.0831
P. tesselatus	Asp	Flat	2	0	0.0000	0.0000	0.0000
P. tesselatus	Asp	North: [0, 45] ∪]316, 360]	48	22	0.4583	1.0711	0.0662
P. tesselatus	Asp	East:]45, 135]	29	14	0.4828	0.6877	0.0896
P. tesselatus	Asp	South:]135, 225]	34	8	0.2353	0.6541	0.0404
P. tesselatus	Asp	West:]225, 315]	37	13	0.3514	0.6756	0.0578
P. tesselatus	Tmed	19	30	11	0.3667	0.6687	0.0669
P. tesselatus	Tmed	21	67	29	0.4328	0.9410	0.0529
P. tesselatus	Tmed	24	14	3	0.2143	0.8018	0.0573
P. tesselatus	Tmed	26	38	14	0.3684	0.7136	0.0598
P. tesselatus	Tmed	28	1	0	0.0000	NA	NA
P. tesselatus	Prec	5	33	4	0.1212	0.5453	0.0949
P. tesselatus	Prec	10	20	13	0.6500	0.8751	0.1957
P. tesselatus	Prec	25	38	13	0.3421	0.9380	0.1522
P. tesselatus	Prec	50	59	27	0.4576	0.8163	0.1063
P. tesselatus	OlivDist	[0, 50]	62	12	0.1935	0.5680	0.0246
P. tesselatus	OlivDist	]50, 100]	25	8	0.3200	0.6272	0.0640
P. tesselatus	OlivDist	]100, 250]	28	12	0.4286	0.5727	0.0810
P. tesselatus	OlivDist	]250, 1000]	30	24	0.8000	1.3493	0.1461
P. tesselatus	OlivDist	> 1000	5	1	0.2000	0.4472	0.0894
P. tesselatus	Oliv250	0	37	28	0.7568	1.2339	0.1244
P. tesselatus	Oliv250	]0, 25]	47	7	0.1489	0.4159	0.0217
P. tesselatus	Oliv250	]25, 50]	29	12	0.4138	0.6823	0.0768
P. tesselatus	Oliv250	]50, 75]	17	4	0.2353	0.7524	0.0571
P. tesselatus	Oliv250	]75, 100]	17	6	0.3529	0.6063	0.0856
P. tesselatus	Oliv250	100	3	0	0.0000	0.0000	0.0000
P. tesselatus	Oliv500	0	19	17	0.8947	1.3701	0.2053
P. tesselatus	Oliv500	]0, 25]	68	28	0.4118	0.8147	0.0499
P. tesselatus	Oliv500	]25, 50]	34	5	0.1471	0.3595	0.0252
P. tesselatus	Oliv500	]50, 75]	22	4	0.1818	0.5011	0.0388
P. tesselatus	Oliv500	]75, 100]	7	3	0.4286	0.7868	0.1620
P. tesselatus	Oliv500	100	0	-	-	-	-

Table F.1 (cont.) – Summary of abundance of different species of *Xylella fastidiosa* vectors and potential vectors (dependent variable) collected in Alentejo Region during spring of 2017 by 22 environmental factors (independent variable). N = number of samples in each class; Sum = total number of insect vectors; Mean = mean abundance of insect vectors; SD = standard deviation of insect vectors; SE = standard error of the mean. Presence of vectors highlighted in grey

Dependent variable	Independent variable	Class	N	Sum	Mean	SD	SE
P. tesselatus	Oliv1000	0	9	4	0.4444	0.7265	0.1481
P. tesselatus	Oliv1000	]0, 25]	83	38	0.4578	0.9791	0.0503
P. tesselatus	Oliv1000	]25, 50]	40	10	0.2500	0.4935	0.0395
P. tesselatus	Oliv1000	]50, 75]	17	5	0.2941	0.5879	0.0713
P. tesselatus	Oliv1000	]75, 100]	1	0	0.0000	NA	NA
P. tesselatus	Oliv1000	100	0	-	-	-	-
P. tesselatus	DistRip	[0, 50]	2	0	0.0000	0.0000	0.0000
P. tesselatus	DistRip	]50, 100]	0	-	-	-	-
P. tesselatus	DistRip	]100, 250]	1	0	0.0000	NA	NA
P. tesselatus	DistRip	]250, 1000]	27	9	0.3333	0.6202	0.0642
P. tesselatus	DistRip	> 1000	120	48	0.4000	0.8638	0.0365
P. tesselatus	Rip250	0	145	53	0.3655	0.8149	0.0304
P. tesselatus	Rip250	]0, 25]	5	4	0.8000	0.8367	0.3578
P. tesselatus	Rip250	]25, 50]	0	-	-	-	-
P. tesselatus	Rip250	]50, 75]	0	-	-	-	-
P. tesselatus	Rip250	]75, 100]	0	-	-	-	-
P. tesselatus	Rip250	100	0	-	-	-	-
P. tesselatus	Rip500	0	137	51	0.3723	0.8225	0.0318
P. tesselatus	Rip500	]0, 25]	13	6	0.4615	0.7763	0.1280
P. tesselatus	Rip500	]25, 50]	0	-	-	-	-
P. tesselatus	Rip500	]50, 75]	0	-	-	-	-
P. tesselatus	Rip500	]75, 100]	0	-	-	-	-
P. tesselatus	Rip500	100	0	-	-	-	-
P. tesselatus	Rip1000	0	122	48	0.3934	0.8582	0.0356
P. tesselatus	Rip1000	]0, 25]	28	9	0.3214	0.6118	0.0607
P. tesselatus	Rip1000	]25, 50]	0	-	-	-	-
P. tesselatus	Rip1000	]50, 75]	0	-	-	-	-
P. tesselatus	Rip1000	]75, 100]	0	-	-	-	-
P. tesselatus	Rip1000	100	0	-	-	-	-
P. tesselatus	Vine250	0	133	49	0.3684	0.8116	0.0319
P. tesselatus	Vine250	]0, 25]	13	8	0.6154	0.9608	0.1707
P. tesselatus	Vine250	]25, 50]	4	0	0.0000	0.0000	0.0000
P. tesselatus	Vine250	]50, 75]	0	-	-	-	-
P. tesselatus	Vine250	]75, 100]	0	-	-	-	-
P. tesselatus	Vine250	100	0	-	-	-	-
P. tesselatus	Past250	0	70	32	0.4571	0.8795	0.0546
P. tesselatus	Past250	]0, 25]	58	13	0.2241	0.5936	0.0294
P. tesselatus	Past250	]25, 50]	16	10	0.6250	1.2042	0.1563
P. tesselatus	Past250	]50, 75]	6	2	0.3333	0.5164	0.1361
P. tesselatus	Past250	]75, 100]	0	-	-	-	-
P. tesselatus	Past250	100	0	-	-	-	-
P. tesselatus	Holm250	0	114	34	0.2982	0.6086	0.0279
P. tesselatus	Holm250	]0, 25]	26	10	0.3846	0.8038	0.0754
P. tesselatus	Holm250	]25, 50]	2	5	2.5000	3.5355	1.7678
P. tesselatus	Holm250	]50, 75]	6	6	1	1,6733	0,4082
P. tesselatus	Holm250	]75, 100]	2	2	1	1,4142	0,7071
P. tesselatus	Holm250	100	0	-	-	-	-
P. tesselatus	Cork250	0	122	47	0.3852	0.8277	0.0349
P. tesselatus	Cork250	]0, 25]	25	8	0.3200	0.8021	0.0640
P. tesselatus	Cork250	]25, 50]	3	2	0.6667	0.5774	0.3849
P. tesselatus	Cork250	]50, 75]	0	-	-	-	-
P. tesselatus	Cork250	]75, 100]	0	-	-	-	-
P. tesselatus	Cork250	100	0	-	-	-	-

Table F.2 – Results of Kruskal-Wallis tests comparing the variation of abundance of different species of *Xylella fastidiosa* vectors among classes from multiple environmental variables. N = number of samples; df = degrees of freedom; χ^2 = Kruskal-Wallis test statistic. Statistically significant results (p-value ≤ 0.05) are highlighted in grey.

Dependent variable	Independent variable	N	df	χ^2	p-value
Lepyronia coleoptrata	Geographic unit	150	17	45.1782	0.0002
Lepyronia coleoptrata	Host plant	150	1	3.2852	0.0699
Lepyronia coleoptrata	Plant family	170	12	22.8626	0.0289
Lepyronia coleoptrata	Plant genus	159	25	21.2618	0.6779
Lepyronia coleoptrata	Plant species	151	29	21.6331	0.8351
Lepyronia coleoptrata	Distance to water masses	150	4	7.1388	0.1287
Lepyronia coleoptrata	Aspect	150	4	4.2787	0.3696
Lepyronia coleoptrata	Altitude	150	4	2.8199	0.5884
Lepyronia coleoptrata	Mean temperature	149	3	1.0798	0.7820
Lepyronia coleoptrata	Total precipitation	150	3	3.7488	0.2899
Lepyronia coleoptrata	Distance to olive groves	150	4	1.9010	0.7540
Lepyronia coleoptrata	Area of olive groves in 250 m radius	150	5	2.1967	0.8213
Lepyronia coleoptrata	Area of olive groves in 500 m radius	150	4	2.4281	0.6576
Lepyronia coleoptrata	Area of olive groves in 1000 m radius	150	4	0.7839	0.9406
Lepyronia coleoptrata	Distance to riparian zones	150	3	0.5034	0.9181
Lepyronia coleoptrata	Area of riparian zones in 250 m radius	150	1	0.0694	0.7922
Lepyronia coleoptrata	Area of riparian zones in 500 m radius	150	1	0.1911	0.6620
Lepyronia coleoptrata	Area of riparian zones in 1000 m radius	150	1	0.4621	0.4966
Lepyronia coleoptrata	Area of vineyards in 250 m radius	150	2	0.2574	0.8793
Lepyronia coleoptrata	Area of pastures in 250 m radius	150	3	0.3670	0.9470
Lepyronia coleoptrata	Area of holm oak in 250 m radius	150	4	0.6358	0.9590
Lepyronia coleoptrata	Area of cork oak in 250 m radius	150	2	0.4621	0.7937
Neophilaenus campestris	Geographic unit	150	17	11.6215	0.8225
Neophilaenus campestris	Host plant	150	1	0.7066	0.4006
Neophilaenus campestris	Plant family	170	12	14.4546	0.2726
Neophilaenus campestris	Plant genus	159	25	13.4546	0.9704
Neophilaenus campestris	Plant species	151	29	15.7778	0.9780
Neophilaenus campestris	Distance to water masses	150	4	6.6726	0.1542
Neophilaenus campestris	Aspect	150	4	1.4963	0.8273
Neophilaenus campestris	Altitude	150	4	5.2823	0.2595
Neophilaenus campestris	Mean temperature	149	3	7.0431	0.0705
Neophilaenus campestris	Total precipitation	150	3	1.1051	0.7758
Neophilaenus campestris	Distance to olive groves	150	4	6.5013	0.1647
Neophilaenus campestris	Area of olive groves in 250 m radius	150	5	1.8814	0.8653
Neophilaenus campestris	Area of olive groves in 500 m radius	150	4	3.0223	0.5541
Neophilaenus campestris	Area of olive groves in 1000 m radius	150	4	2.6181	0.6236
Neophilaenus campestris	Distance to riparian zones	150	3	0.1142	0.9901
Neophilaenus campestris	Area of riparian zones in 250 m radius	150	1	0.1772	0.6738
Neophilaenus campestris	Area of riparian zones in 500 m radius	150	1	0.4875	0.4850
Neophilaenus campestris	Area of riparian zones in 1000 m radius	150	1	0.0060	0.9382
Neophilaenus campestris	Area of vineyards in 250 m radius	150	2	6.2775	0.0433
Neophilaenus campestris	Area of pastures in 250 m radius	150	3	3.8066	0.2831
Neophilaenus campestris	Area of holm oak in 250 m radius	150	4	2.0385	0.7287
Neophilaenus campestris	Area of cork oak in 250 m radius	150	2	6.9707	0.0306
Philaenus sp.	Geographic unit	150	17	37.7143	0.0027
Philaenus sp.	Host plant	150	1	5.0067	0.0252
Philaenus sp.	Plant family	170	12	4.4980	0.9727
Philaenus sp.	Plant genus	159	25	30.6860	0.1996
Philaenus sp.	Plant species	151	29	31.6637	0.3348
Philaenus sp.	Distance to water masses	150	4	5.6615	0.2259
Philaenus sp.	Aspect	150	4	3.6463	0.4560
Philaenus sp.	Altitude	150	4	2.4550	0.6527
Philaenus sp.	Mean temperature	149	3	16.7240	0.0008
Philaenus sp.	Total precipitation	150	3	6.1720	0.1035

Table F.2 (cont.) – Results of Kruskal-Wallis tests comparing the variation of abundance of different species of *Xylella fastidiosa* vectors among classes from multiple environmental variables. N = number of samples; df = degrees of freedom; χ^2 = Kruskal-Wallis test statistic. Statistically significant results (p-value ≤ 0.05) are highlighted in grey.

Dependent variable	Independent variable	N	df	χ^2	p-value
Philaenus sp.	Distance to olive groves	150	4	6.1600	0.1875
Philaenus sp.	Area of olive groves in 250 m radius	150	5	14.8527	0.0110
Philaenus sp.	Area of olive groves in 500 m radius	150	4	5.4434	0.2447
Philaenus sp.	Area of olive groves in 1000 m radius	150	4	1.9569	0.7437
Philaenus sp.	Distance to riparian zones	150	3	0.4223	0.9356
Philaenus sp.	Area of riparian zones in 250 m radius	150	1	0.2892	0.5907
Philaenus sp.	Area of riparian zones in 500 m radius	150	1	2.8271	0.0927
Philaenus sp.	Area of riparian zones in 1000 m radius	150	1	0.2216	0.6378
Philaenus sp.	Area of vineyards in 250 m radius	150	2	1.0722	0.5850
Philaenus sp.	Area of pastures in 250 m radius	150	3	5.2805	0.1524
Philaenus sp.	Area of holm oak in 250 m radius	150	4	2.6489	0.6182
Philaenus sp.	Area of cork oak in 250 m radius	150	2	0.5833	0.7470
Philaenus spumarius	Geographic unit	150	17	17.7500	0.4048
Philaenus spumarius	Host plant	150	1	1.6316	0.2015
Philaenus spumarius	Plant family	170	12	3.5946	0.9897
Philaenus spumarius	Plant genus	159	25	6.5714	0.9999
Philaenus spumarius	Plant species	151	29	8.4375	0.9999
Philaenus spumarius	Distance to water masses	150	4	4.7692	0.3118
Philaenus spumarius	Aspect	150	4	2.1250	0.7128
Philaenus spumarius	Altitude	150	4	20.4286	0.0004
Philaenus spumarius	Mean temperature	149	3	9.6429	0.0219
Philaenus spumarius	Total precipitation	150	3	3.5455	0.3149
Philaenus spumarius	Distance to olive groves	150	4	1.4194	0.8408
Philaenus spumarius	Area of olive groves in 250 m radius	150	5	2.1915	0.8221
Philaenus spumarius	Area of olive groves in 500 m radius	150	4	1.2059	0.8771
Philaenus spumarius	Area of olive groves in 1000 m radius	150	4	0.8072	0.9375
Philaenus spumarius	Distance to riparian zones	150	3	0.2500	0.9691
Philaenus spumarius	Area of riparian zones in 250 m radius	150	1	0.0345	0.8527
Philaenus spumarius	Area of riparian zones in 500 m radius	150	1	0.0949	0.7580
Philaenus spumarius	Area of riparian zones in 1000 m radius	150	1	0.2295	0.6319
Philaenus spumarius	Area of vineyards in 250 m radius	150	2	0.1278	0.9381
Philaenus spumarius	Area of pastures in 250 m radius	150	3	1.1429	0.7667
Philaenus spumarius	Area of holm oak in 250 m radius	150	4	0.3158	0.9888
Philaenus spumarius	Area of cork oak in 250 m radius	150	2	5.0000	0.0821
Philaenus tesselatus	Geographic unit	150	17	25.8363	0.0775
Philaenus tesselatus	Host plant	150	1	0.6883	0.4067
Philaenus tesselatus	Plant family	170	12	3.7336	0.9878
Philaenus tesselatus	Plant genus	159	25	24.8088	0.4731
Philaenus tesselatus	Plant species	151	29	26.4916	0.5991
Philaenus tesselatus	Distance to water masses	150	4	4.2757	0.3700
Philaenus tesselatus	Aspect	150	4	4.7372	0.3153
Philaenus tesselatus	Altitude	150	4	4.4363	0.3502
Philaenus tesselatus	Mean temperature	149	3	2.0011	0.5722
Philaenus tesselatus	Total precipitation	150	3	11.7718	0.0082
Philaenus tesselatus	Distance to olive groves	150	4	9.1654	0.0571
Philaenus tesselatus	Area of olive groves in 250 m radius	150	5	11.3933	0.0441
Philaenus tesselatus	Area of olive groves in 500 m radius	150	4	8.1135	0.0875
Philaenus tesselatus	Area of olive groves in 1000 m radius	150	4	0.9383	0.9190
Philaenus tesselatus	Distance to riparian zones	150	3	0.9487	0.8137
Philaenus tesselatus	Area of riparian zones in 250 m radius	150	1	3.3223	0.0683
Philaenus tesselatus	Area of riparian zones in 500 m radius	150	1	0.3921	0.5312
Philaenus tesselatus	Area of riparian zones in 1000 m radius	150	1	0.0007	0.9794
Philaenus tesselatus	Area of vineyards in 250 m radius	150	2	2.7840	0.2486
Philaenus tesselatus	Area of pastures in 250 m radius	150	3	3.8948	0.2730

Table F.2 (cont.) – Results of Kruskal-Wallis tests comparing the variation of abundance of different species of *Xylella fastidiosa* vectors among classes from multiple environmental variables. N = number of samples; df = degrees of freedom; χ^2 = Kruskal-Wallis test statistic. Statistically significant results (p-value ≤ 0.05) are highlighted in grey.

Dependent variable	Independent variable	N	df	χ^2	p-value
Philaenus tesselatus	Area of holm oak in 250 m radius	150	4	3.5637	0.4683
Philaenus tesselatus	Area of cork oak in 250 m radius	150	2	2.7277	0.2557

Table F.3 – Results of one-way ANOVA tests comparing ranked abundances of different species of *Xylella fastidiosa* vectors (dependent variable) among classes of environmental factors (independent variable) with more than two classes that showed statistically significant differences (p-value ≤ 0.05) in Kruskal-Wallis tests previously applied to data of raw abundances. SS = sum of squares; MS = Mean sum of squares; df = degrees of freedom; F-value = F test statistic.

Dependent variable	Independent variable	Source	SS	MS	df	F-value	p-value
Lepyronia coleoptrata	Geographic unit	Between groups	3366	197.98	17	3.379	<0.0001
		Within groups	7734	58.59	132		
	Plant family	Between groups	2118	176.49	12	2.047	0.0235
		Within groups	13538	86.23	157		
Neophilaenus campestris	Area of vineyards in 250 m radius	Between groups	1145	572.70	2	3.233	0.0423
		Within groups	26042	177.20	147		
	Area of cork oak in 250 m radius	Between groups	1272	636.00	2	3.607	0.0296
		Within groups	25916	176.30	147		
Philaenus sp.	Geographic unit	Between groups	10791	634.70	17	2.631	0.0011
		Within groups	31841	241.20	132		
	Mean temperature	Between groups	4816	16055.00	3	6159	<0.0001
		Within groups	37799	2607.00	145		
	Area of olive groves in 250 m radius	Between groups	4250	849.90	5	3.189	0.0092
		Within groups	38382	266.50	144		
Philaenus tesselatus	Total precipitation	Between groups	12389	4130.00	3	4.175	0.0072
		Within groups	144427	989.00	146		
	Area of olive groves in 250 m radius	Between groups	11991	2398.00	5	2.385	0.0411
		Within groups	144826	1006.00	144		

Table F.4 – Results of Fisher's LSD tests comparing ranked abundances of different species of *Xylella fastidiosa* vectors (dependent variable) among classes of environmental factors (independent variable) that showed statistically significant differences (p-value ≤ 0.05) in the one-way ANOVA previously applied. I = class *i* of corresponding independent variable; J = class *j* of corresponding independent variable; I-J = mean difference of ranked abundances between class *i* and class *j*; SE = standard error of I-J; LCL = lower bound of 95% confidence interval; UCL = upper bound of 95% confidence interval; t-value = Fisher's LSD test statistic; df = degrees of freedom. Statistically significant differences (p-value ≤ 0.05) are highlighted in grey.

Dependent variabe	Independent variable	I	J	I-J	SE	LCI	UCI	t-value	df	p-value
L. coleoptrata	GU	0	1	0.0000	5.1822	-10.2510	10.2510	0.0000	132	1.0000
L. coleoptrata	GU	0	2	0.0000	3.3926	-6.7108	6.7108	0.0000	132	1.0000
L. coleoptrata	GU	0	3	-37.5000	6.0515	-49.4705	-25.5295	6.1968	132	<0.0001
L. coleoptrata	GU	0	4	0.0000	6.0515	-11.9705	11.9705	0.0000	132	1.0000
L. coleoptrata	GU	0	6	0.0000	3.8273	-7.5708	7.5708	0.0000	132	1.0000
L. coleoptrata	GU	0	7	0.0000	6.0515	-11.9705	11.9705	0.0000	132	1.0000
L. coleoptrata	GU	0	8	0.0000	3.3926	-6.7108	6.7108	0.0000	132	1.0000
L. coleoptrata	GU	0	9	0.0000	3.3926	-6.7108	6.7108	0.0000	132	1.0000
L. coleoptrata	GU	0	13	0.0000	3.7195	-7.3575	7.3575	0.0000	132	1.0000
L. coleoptrata	GU	0	14	0.0000	3.9617	-7.8366	7.8366	0.0000	132	1.0000
L. coleoptrata	GU	0	15	0.0000	3.3926	-6.7108	6.7108	0.0000	132	1.0000
L. coleoptrata	GU	0	19	0.0000	3.7195	-7.3575	7.3575	0.0000	132	1.0000
L. coleoptrata	GU	0	20	0.0000	3.7195	-7.3575	7.3575	0.0000	132	1.0000
L. coleoptrata	GU	0	21	-9.3750	3.8273	-16.9458	-1.8042	2.4495	132	0.0156
L. coleoptrata	GU	0	25	0.0000	3.8273	-7.5708	7.5708	0.0000	132	1.0000
L. coleoptrata	GU	0	26	0.0000	3.7195	-7.3575	7.3575	0.0000	132	1.0000
L. coleoptrata	GU	0	27	0.0000	3.6309	-7.1823	7.1823	0.0000	132	1.0000
L. coleoptrata	GU	1	2	0.0000	4.8700	-9.6333	9.6333	0.0000	132	1.0000

Table F.4 (cont.) – Results of Fisher's LSD tests comparing ranked abundances of different species of *Xylella fastidiosa* vectors (dependent variable) among classes of environmental factors (independent variable) that showed statistically significant differences (p-value ≤ 0.05) in the one-way ANOVA previously applied. I = class *i* of corresponding independent variable; J = class *j* of corresponding independent variable; I-J = mean difference of ranked abundances between class *i* and class *j*; SE = standard error of I-J; LCL = lower bound of 95% confidence interval; UCL = upper bound of 95% confidence interval; t-value = Fisher's LSD test statistic; df = degrees of freedom. Statistically significant differences (p-value ≤ 0.05) are highlighted in grey.

Dependent variable	Independent variable	I	J	I-J	SE	LCI	UCI	t-value	df	p-value
L. coleoptrata	GU	1	3	-37.5000	6.9877	-51.3224	-23.6776	5.3666	132	<0.0001
L. coleoptrata	GU	1	4	0.0000	6.9877	-13.8224	13.8224	0.0000	132	1.0000
L. coleoptrata	GU	1	6	0.0000	5.1822	-10.2510	10.2510	0.0000	132	1.0000
L. coleoptrata	GU	1	7	0.0000	6.9877	-13.8224	13.8224	0.0000	132	1.0000
L. coleoptrata	GU	1	8	0.0000	4.8700	-9.6333	9.6333	0.0000	132	1.0000
L. coleoptrata	GU	1	9	0.0000	4.8700	-9.6333	9.6333	0.0000	132	1.0000
L. coleoptrata	GU	1	13	0.0000	5.1031	-10.0944	10.0944	0.0000	132	1.0000
L. coleoptrata	GU	1	14	0.0000	5.2822	-10.4487	10.4487	0.0000	132	1.0000
L. coleoptrata	GU	1	15	0.0000	4.8700	-9.6333	9.6333	0.0000	132	1.0000
L. coleoptrata	GU	1	19	0.0000	5.1031	-10.0944	10.0944	0.0000	132	1.0000
L. coleoptrata	GU	1	20	0.0000	5.1031	-10.0944	10.0944	0.0000	132	1.0000
L. coleoptrata	GU	1	21	-9.3750	5.1822	-19.6260	0.8760	1.8091	132	0.0727
L. coleoptrata	GU	1	25	0.0000	5.1822	-10.2510	10.2510	0.0000	132	1.0000
L. coleoptrata	GU	1	26	0.0000	5.1031	-10.0944	10.0944	0.0000	132	1.0000
L. coleoptrata	GU	1	27	0.0000	5.0389	-9.9675	9.9675	0.0000	132	1.0000
L. coleoptrata	GU	2	3	-37.5000	5.7864	-48.9460	-26.054	6.4807	132	<0.0001
L. coleoptrata	GU	2	4	0.0000	5.7864	-11.4460	11.4460	0.0000	132	1.0000
L. coleoptrata	GU	2	6	0.0000	3.3926	-6.7108	6.7108	0.0000	132	1.0000
L. coleoptrata	GU	2	7	0.0000	5.7864	-11.4460	11.4460	0.0000	132	1.0000
L. coleoptrata	GU	2	8	0.0000	2.8932	-5.7230	5.7230	0.0000	132	1.0000
L. coleoptrata	GU	2	9	0.0000	2.8932	-5.7230	5.7230	0.0000	132	1.0000
L. coleoptrata	GU	2	13	0.0000	3.2704	-6.4692	6.4692	0.0000	132	1.0000
L. coleoptrata	GU	2	14	0.0000	3.5434	-7.0092	7.0092	0.0000	132	1.0000
L. coleoptrata	GU	2	15	0.0000	2.8932	-5.7230	5.7230	0.0000	132	1.0000
L. coleoptrata	GU	2	19	0.0000	3.2704	-6.4692	6.4692	0.0000	132	1.0000
L. coleoptrata	GU	2	20	0.0000	3.2704	-6.4692	6.4692	0.0000	132	1.0000
L. coleoptrata	GU	2	21	-9.3750	3.3926	-16.0858	-2.6642	2.7634	132	0.0065
L. coleoptrata	GU	2	25	0.0000	3.3926	-6.7108	6.7108	0.0000	132	1.0000
L. coleoptrata	GU	2	26	0.0000	3.2704	-6.4692	6.4692	0.0000	132	1.0000
L. coleoptrata	GU	2	27	0.0000	3.1693	-6.2692	6.2692	0.0000	132	1.0000
L. coleoptrata	GU	3	4	37.5000	7.6547	22.3583	52.6417	4.8990	132	<0.0001
L. coleoptrata	GU	3	6	37.5000	6.0515	25.5295	49.4705	6.1968	132	<0.0001
L. coleoptrata	GU	3	7	37.5000	7.6547	22.3583	52.6417	4.8990	132	<0.0001
L. coleoptrata	GU	3	8	37.5000	5.7864	26.0540	48.9460	6.4807	132	<0.0001
L. coleoptrata	GU	3	9	37.5000	5.7864	26.0540	48.9460	6.4807	132	<0.0001
L. coleoptrata	GU	3	13	37.5000	5.9839	-49.3368	-25.6632	6.2668	132	<0.0001
L. coleoptrata	GU	3	14	37.5000	6.1374	-49.6403	-25.3597	6.1101	132	<0.0001
L. coleoptrata	GU	3	15	37.5000	5.7864	-48.9460	-26.0540	6.4807	132	<0.0001
L. coleoptrata	GU	3	19	37.5000	5.9839	-49.3368	-25.6632	6.2668	132	<0.0001
L. coleoptrata	GU	3	20	37.5000	5.9839	-49.3368	-25.6632	6.2668	132	<0.0001
L. coleoptrata	GU	3	21	28.1250	6.0515	-40.0955	-16.1545	4.6476	132	<0.0001
L. coleoptrata	GU	3	25	37.5000	6.0515	-49.4705	-25.5295	6.1968	132	<0.0001
L. coleoptrata	GU	3	26	37.5000	5.9839	-49.3368	-25.6632	6.2668	132	<0.0001
L. coleoptrata	GU	3	27	37.5000	5.9293	-49.2287	-25.7713	6.3246	132	<0.0001
L. coleoptrata	GU	4	6	0.0000	6.0515	-11.9705	11.9705	0.0000	132	1.0000
L. coleoptrata	GU	4	7	0.0000	7.6547	-15.1417	15.1417	0.0000	132	1.0000
L. coleoptrata	GU	4	8	0.0000	5.7864	-11.4460	11.4460	0.0000	132	1.0000
L. coleoptrata	GU	4	9	0.0000	5.7864	-11.4460	11.4460	0.0000	132	1.0000
L. coleoptrata	GU	4	13	0.0000	5.9839	-11.8368	11.8368	0.0000	132	1.0000
L. coleoptrata	GU	4	14	0.0000	6.1374	-12.1403	12.1403	0.0000	132	1.0000

Table F.4 (cont.) – Results of Fisher's LSD tests comparing ranked abundances of different species of *Xylella fastidiosa* vectors (dependent variable) among classes of environmental factors (independent variable) that showed statistically significant differences (p-value ≤ 0.05) in the one-way ANOVA previously applied. I = class *i* of corresponding independent variable; J = class *j* of corresponding independent variable; I-J = mean difference of ranked abundances between class *i* and class *j*; SE = standard error of I-J; LCL = lower bound of 95% confidence interval; UCL = upper bound of 95% confidence interval; t-value = Fisher's LSD test statistic; df = degrees of freedom. Statistically significant differences (p-value ≤ 0.05) are highlighted in grey.

Dependent variable	Independent variable	I	J	I-J	SE	LCI	UCI	t-value	df	p-value
L. coleoptrata	GU	4	15	0.0000	5.7864	-11.4460	11.4460	0.0000	132	1.0000
L. coleoptrata	GU	4	19	0.0000	5.9839	-11.8368	11.8368	0.0000	132	1.0000
L. coleoptrata	GU	4	20	0.0000	5.9839	-11.8368	11.8368	0.0000	132	1.0000
L. coleoptrata	GU	4	21	-9.3750	6.0515	-2.5955	21.3455	1.5492	132	0.1237
L. coleoptrata	GU	4	25	0.0000	6.0515	-11.9705	11.9705	0.0000	132	1.0000
L. coleoptrata	GU	4	26	0.0000	5.9839	-11.8368	11.8368	0.0000	132	1.0000
L. coleoptrata	GU	4	27	0.0000	5.9293	-11.7287	11.7287	0.0000	132	1.0000
L. coleoptrata	GU	6	7	0.0000	6.0515	-11.9705	11.9705	0.0000	132	1.0000
L. coleoptrata	GU	6	8	0.0000	3.3926	-6.7108	6.7108	0.0000	132	1.0000
L. coleoptrata	GU	6	9	0.0000	3.3926	-6.7108	6.7108	0.0000	132	1.0000
L. coleoptrata	GU	6	13	0.0000	3.7195	-7.3575	7.3575	0.0000	132	1.0000
L. coleoptrata	GU	6	14	0.0000	3.9617	-7.8366	7.8366	0.0000	132	1.0000
L. coleoptrata	GU	6	15	0.0000	3.3926	-6.7108	6.7108	0.0000	132	1.0000
L. coleoptrata	GU	6	19	0.0000	3.7195	-7.3575	7.3575	0.0000	132	1.0000
L. coleoptrata	GU	6	20	0.0000	3.7195	-7.3575	7.3575	0.0000	132	1.0000
L. coleoptrata	GU	6	21	-9.3750	3.8273	1.8042	16.9458	2.4495	132	0.0156
L. coleoptrata	GU	6	25	0.0000	3.8273	-7.5708	7.5708	0.0000	132	1.0000
L. coleoptrata	GU	6	26	0.0000	3.7195	-7.3575	7.3575	0.0000	132	1.0000
L. coleoptrata	GU	6	27	0.0000	3.6309	-7.1823	7.1823	0.0000	132	1.0000
L. coleoptrata	GU	7	8	0.0000	5.7864	-11.4460	11.4460	0.0000	132	1.0000
L. coleoptrata	GU	7	9	0.0000	5.7864	-11.4460	11.4460	0.0000	132	1.0000
L. coleoptrata	GU	7	13	0.0000	5.9839	-11.8368	11.8368	0.0000	132	1.0000
L. coleoptrata	GU	7	14	0.0000	6.1374	-12.1403	12.1403	0.0000	132	1.0000
L. coleoptrata	GU	7	15	0.0000	5.7864	-11.4460	11.4460	0.0000	132	1.0000
L. coleoptrata	GU	7	19	0.0000	5.9839	-11.8368	11.8368	0.0000	132	1.0000
L. coleoptrata	GU	7	20	0.0000	5.9839	-11.8368	11.8368	0.0000	132	1.0000
L. coleoptrata	GU	7	21	-9.3750	6.0515	-2.5955	21.3455	1.5492	132	0.1237
L. coleoptrata	GU	7	25	0.0000	6.0515	-11.9705	11.9705	0.0000	132	1.0000
L. coleoptrata	GU	7	26	0.0000	5.9839	-11.8368	11.8368	0.0000	132	1.0000
L. coleoptrata	GU	7	27	0.0000	5.9293	-11.7287	11.7287	0.0000	132	1.0000
L. coleoptrata	GU	8	9	0.0000	2.8932	-5.7230	5.7230	0.0000	132	1.0000
L. coleoptrata	GU	8	13	0.0000	3.2704	-6.4692	6.4692	0.0000	132	1.0000
L. coleoptrata	GU	8	14	0.0000	3.5434	-7.0092	7.0092	0.0000	132	1.0000
L. coleoptrata	GU	8	15	0.0000	2.8932	-5.7230	5.7230	0.0000	132	1.0000
L. coleoptrata	GU	8	19	0.0000	3.2704	-6.4692	6.4692	0.0000	132	1.0000
L. coleoptrata	GU	8	20	0.0000	3.2704	-6.4692	6.4692	0.0000	132	1.0000
L. coleoptrata	GU	8	21	-9.3750	3.3926	2.6642	16.0858	2.7634	132	0.0065
L. coleoptrata	GU	8	25	0.0000	3.3926	-6.7108	6.7108	0.0000	132	1.0000
L. coleoptrata	GU	8	26	0.0000	3.2704	-6.4692	6.4692	0.0000	132	1.0000
L. coleoptrata	GU	8	27	0.0000	3.1693	-6.2692	6.2692	0.0000	132	1.0000
L. coleoptrata	GU	9	13	0.0000	3.2704	-6.4692	6.4692	0.0000	132	1.0000
L. coleoptrata	GU	9	14	0.0000	3.5434	-7.0092	7.0092	0.0000	132	1.0000
L. coleoptrata	GU	9	15	0.0000	2.8932	-5.7230	5.7230	0.0000	132	1.0000
L. coleoptrata	GU	9	19	0.0000	3.2704	-6.4692	6.4692	0.0000	132	1.0000
L. coleoptrata	GU	9	20	0.0000	3.2704	-6.4692	6.4692	0.0000	132	1.0000
L. coleoptrata	GU	9	21	-9.3750	3.3926	2.6642	16.0858	2.7634	132	0.0065
L. coleoptrata	GU	9	25	0.0000	3.3926	-6.7108	6.7108	0.0000	132	1.0000
L. coleoptrata	GU	9	26	0.0000	3.2704	-6.4692	6.4692	0.0000	132	1.0000
L. coleoptrata	GU	9	27	0.0000	3.1693	-6.2692	6.2692	0.0000	132	1.0000
L. coleoptrata	GU	13	14	0.0000	3.8576	-7.6307	7.6307	0.0000	132	1.0000

Table F.4 (cont.) – Results of Fisher's LSD tests comparing ranked abundances of different species of *Xylella fastidiosa* vectors (dependent variable) among classes of environmental factors (independent variable) that showed statistically significant differences (p-value ≤ 0.05) in the one-way ANOVA previously applied. I = class *i* of corresponding independent variable; J = class *j* of corresponding independent variable; I-J = mean difference of ranked abundances between class *i* and class *j*; SE = standard error of I-J; LCL = lower bound of 95% confidence interval; UCL = upper bound of 95% confidence interval; t-value = Fisher's LSD test statistic; df = degrees of freedom. Statistically significant differences (p-value ≤ 0.05) are highlighted in grey.

Dependent variable	Independent variable	I	J	I-J	SE	LCI	UCI	t-value	df	p-value
L. coleoptrata	GU	13	15	0.0000	3.2704	-6.4692	6.4692	0.0000	132	1.0000
L. coleoptrata	GU	13	19	0.0000	3.6084	-7.1378	7.1378	0.0000	132	1.0000
L. coleoptrata	GU	13	20	0.0000	3.6084	-7.1378	7.1378	0.0000	132	1.0000
L. coleoptrata	GU	13	21	-9.3750	3.7195	-16.7325	-2.0175	2.5205	132	0.0129
L. coleoptrata	GU	13	25	0.0000	3.7195	-7.3575	7.3575	0.0000	132	1.0000
L. coleoptrata	GU	13	26	0.0000	3.6084	-7.1378	7.1378	0.0000	132	1.0000
L. coleoptrata	GU	13	27	0.0000	3.5171	-6.9571	6.9571	0.0000	132	1.0000
L. coleoptrata	GU	14	15	0.0000	3.5434	-7.0092	7.0092	0.0000	132	1.0000
L. coleoptrata	GU	14	19	0.0000	3.8576	-7.6307	7.6307	0.0000	132	1.0000
L. coleoptrata	GU	14	20	0.0000	3.8576	-7.6307	7.6307	0.0000	132	1.0000
L. coleoptrata	GU	14	21	-9.3750	3.9617	-17.2116	-1.5384	2.3664	132	0.0194
L. coleoptrata	GU	14	25	0.0000	3.9617	-7.8366	7.8366	0.0000	132	1.0000
L. coleoptrata	GU	14	26	0.0000	3.8576	-7.6307	7.6307	0.0000	132	1.0000
L. coleoptrata	GU	14	27	0.0000	3.7723	-7.4619	7.4619	0.0000	132	1.0000
L. coleoptrata	GU	15	19	0.0000	3.2704	-6.4692	6.4692	0.0000	132	1.0000
L. coleoptrata	GU	15	20	0.0000	3.2704	-6.4692	6.4692	0.0000	132	1.0000
L. coleoptrata	GU	15	21	-9.3750	3.3926	-16.0858	-2.6642	2.7634	132	0.0065
L. coleoptrata	GU	15	25	0.0000	3.3926	-6.7108	6.7108	0.0000	132	1.0000
L. coleoptrata	GU	15	26	0.0000	3.2704	-6.4692	6.4692	0.0000	132	1.0000
L. coleoptrata	GU	15	27	0.0000	3.1693	-6.2692	6.2692	0.0000	132	1.0000
L. coleoptrata	GU	19	20	0.0000	3.6084	-7.1378	7.1378	0.0000	132	1.0000
L. coleoptrata	GU	19	21	-9.3750	3.7195	-16.7325	-2.0175	2.5205	132	0.0129
L. coleoptrata	GU	19	25	0.0000	3.7195	-7.3575	7.3575	0.0000	132	1.0000
L. coleoptrata	GU	19	26	0.0000	3.6084	-7.1378	7.1378	0.0000	132	1.0000
L. coleoptrata	GU	19	27	0.0000	3.5171	-6.9571	6.9571	0.0000	132	1.0000
L. coleoptrata	GU	20	21	-9.3750	3.7195	-16.7325	-2.0175	2.5205	132	0.0129
L. coleoptrata	GU	20	25	0.0000	3.7195	-7.3575	7.3575	0.0000	132	1.0000
L. coleoptrata	GU	20	26	0.0000	3.6084	-7.1378	7.1378	0.0000	132	1.0000
L. coleoptrata	GU	20	27	0.0000	3.5171	-6.9571	6.9571	0.0000	132	1.0000
L. coleoptrata	GU	21	25	-9.3750	3.8273	1.8042	16.9458	2.4495	132	0.0156
L. coleoptrata	GU	21	26	-9.3750	3.7195	2.0175	16.7325	2.5205	132	0.0129
L. coleoptrata	GU	21	27	-9.3750	3.6309	2.1927	16.5573	2.5820	132	0.0109
L. coleoptrata	GU	25	26	0.0000	3.7195	-7.3575	7.3575	0.0000	132	1.0000
L. coleoptrata	GU	25	27	0.0000	3.6309	-7.1823	7.1823	0.0000	132	1.0000
L. coleoptrata	GU	26	27	0.0000	3.5171	-6.9571	6.9571	0.0000	132	1.0000
L. coleoptrata	Fam	APIAC	ASTER	0.0000	1.9604	-3.8722	3.8722	0.0000	157	1.0000
L. coleoptrata	Fam	APIAC	BORAG	0.0000	2.6685	-5.2708	5.2708	0.0000	157	1.0000
L. coleoptrata	Fam	APIAC	BRASS	0.0000	4.4245	-8.7392	8.7392	0.0000	157	1.0000
L. coleoptrata	Fam	APIAC	CISTA	0.0000	5.5743	-11.0103	11.0103	0.0000	157	1.0000
L. coleoptrata	Fam	APIAC	CONVO	-8.0909	3.1889	-14.3897	-1.7922	2.5372	157	1.0000
L. coleoptrata	Fam	APIAC	DIPSA	0.0000	4.4245	-8.7392	8.7392	0.0000	157	1.0000
L. coleoptrata	Fam	APIAC	FABAC	0.0000	5.5743	-11.0103	11.0103	0.0000	157	1.0000
L. coleoptrata	Fam	APIAC	GENTI	0.0000	6.7412	-13.3152	13.3152	0.0000	157	1.0000
L. coleoptrata	Fam	APIAC	HYPER	0.0000	6.7412	-13.3152	13.3152	0.0000	157	1.0000
L. coleoptrata	Fam	APIAC	MALVA	0.0000	2.7784	-5.4879	5.4879	0.0000	157	1.0000
L. coleoptrata	Fam	APIAC	PAPAV	0.0000	4.0868	-8.0721	8.0721	0.0000	157	1.0000
L. coleoptrata	Fam	APIAC	SCROP	-17.8000	4.4245	-26.5392	-9.0608	4.0231	157	1.0000
L. coleoptrata	Fam	ASTER	BORAG	0.0000	2.5106	-4.9589	4.9589	0.0000	157	1.0000
L. coleoptrata	Fam	ASTER	BRASS	0.0000	4.3311	-8.5547	8.5547	0.0000	157	1.0000
L. coleoptrata	Fam	ASTER	CISTA	0.0000	5.5005	-10.8645	10.8645	0.0000	157	1.0000

Table F.4 (cont.) – Results of Fisher's LSD tests comparing ranked abundances of different species of *Xylella fastidiosa* vectors (dependent variable) among classes of environmental factors (independent variable) that showed statistically significant differences (p-value ≤ 0.05) in the one-way ANOVA previously applied. I = class *i* of corresponding independent variable; J = class *j* of corresponding independent variable; I-J = mean difference of ranked abundances between class *i* and class *j*; SE = standard error of I-J; LCL = lower bound of 95% confidence interval; UCL = upper bound of 95% confidence interval; t-value = Fisher's LSD test statistic; df = degrees of freedom. Statistically significant differences (p-value ≤ 0.05) are highlighted in grey.

Dependent variable	Independent variable	I	J	I-J	SE	LCI	UCI	t-value	df	p-value
L. coleoptrata	Fam	ASTER	CONVO	-8.0909	3.0580	-14.1311	-2.0507	2.6458	157	1.0000
L. coleoptrata	Fam	ASTER	DIPSA	0.0000	4.3311	-8.5547	8.5547	0.0000	157	1.0000
L. coleoptrata	Fam	ASTER	FABAC	0.0000	5.5005	-10.8645	10.8645	0.0000	157	1.0000
L. coleoptrata	Fam	ASTER	GENTI	0.0000	6.6803	-13.1949	13.1949	0.0000	157	1.0000
L. coleoptrata	Fam	ASTER	HYPER	0.0000	6.6803	-13.1949	13.1949	0.0000	157	1.0000
L. coleoptrata	Fam	ASTER	MALVA	0.0000	2.6272	-5.1891	5.1891	0.0000	157	1.0000
L. coleoptrata	Fam	ASTER	PAPAV	0.0000	3.9855	-7.8721	7.8721	0.0000	157	1.0000
L. coleoptrata	Fam	ASTER	SCROP	-17.8000	4.3311	-26.3547	-9.2453	4.1098	157	1.0000
L. coleoptrata	Fam	BORAG	BRASS	0.0000	4.6942	-9.2720	9.2720	0.0000	157	1.0000
L. coleoptrata	Fam	BORAG	CISTA	0.0000	5.7908	-11.4378	11.4378	0.0000	157	1.0000
L. coleoptrata	Fam	BORAG	CONVO	-8.0909	3.5538	-15.1103	-1.0715	2.2767	157	1.0000
L. coleoptrata	Fam	BORAG	DIPSA	0.0000	4.6942	-9.2720	9.2720	0.0000	157	1.0000
L. coleoptrata	Fam	BORAG	FABAC	0.0000	5.7908	-11.4378	11.4378	0.0000	157	1.0000
L. coleoptrata	Fam	BORAG	GENTI	0.0000	6.9213	-13.6708	13.6708	0.0000	157	1.0000
L. coleoptrata	Fam	BORAG	HYPER	0.0000	6.9213	-13.6708	13.6708	0.0000	157	1.0000
L. coleoptrata	Fam	BORAG	MALVA	0.0000	3.1906	-6.3019	6.3019	0.0000	157	1.0000
L. coleoptrata	Fam	BORAG	PAPAV	0.0000	4.3774	-8.6462	8.6462	0.0000	157	1.0000
L. coleoptrata	Fam	BORAG	SCROP	-17.8000	4.6942	-27.0720	-8.5280	3.7919	157	1.0000
L. coleoptrata	Fam	BRASS	CISTA	0.0000	6.7814	-13.3946	13.3946	0.0000	157	1.0000
L. coleoptrata	Fam	BRASS	CONVO	-8.0909	5.0084	-17.9835	1.8017	1.6155	157	1.0000
L. coleoptrata	Fam	BRASS	DIPSA	0.0000	5.8729	-11.6001	11.6001	0.0000	157	1.0000
L. coleoptrata	Fam	BRASS	FABAC	0.0000	6.7814	-13.3946	13.3946	0.0000	157	1.0000
L. coleoptrata	Fam	BRASS	GENTI	0.0000	7.7691	-15.3455	15.3455	0.0000	157	1.0000
L. coleoptrata	Fam	BRASS	HYPER	0.0000	7.7691	-15.3455	15.3455	0.0000	157	1.0000
L. coleoptrata	Fam	BRASS	MALVA	0.0000	4.7576	-9.3971	9.3971	0.0000	157	1.0000
L. coleoptrata	Fam	BRASS	PAPAV	0.0000	5.6229	-11.1062	11.1062	0.0000	157	1.0000
L. coleoptrata	Fam	BRASS	SCROP	-17.8000	5.8729	-29.4001	-6.1999	3.0309	157	1.0000
L. coleoptrata	Fam	CISTA	CONVO	-8.0909	6.0483	-20.0373	3.8555	1.3377	157	1.0000
L. coleoptrata	Fam	CISTA	DIPSA	0.0000	6.7814	-13.3946	13.3946	0.0000	157	1.0000
L. coleoptrata	Fam	CISTA	FABAC	0.0000	7.5819	-14.9757	14.9757	0.0000	157	1.0000
L. coleoptrata	Fam	CISTA	GENTI	0.0000	8.4768	-16.7433	16.7433	0.0000	157	1.0000
L. coleoptrata	Fam	CISTA	HYPER	0.0000	8.4768	-16.7433	16.7433	0.0000	157	1.0000
L. coleoptrata	Fam	CISTA	MALVA	0.0000	5.8422	-11.5395	11.5395	0.0000	157	1.0000
L. coleoptrata	Fam	CISTA	PAPAV	0.0000	6.5661	-12.9693	12.9693	0.0000	157	1.0000
L. coleoptrata	Fam	CISTA	SCROP	-17.8000	6.7814	-31.1946	-4.4054	2.6248	157	1.0000
L. coleoptrata	Fam	CONVO	DIPSA	8.0909	5.0084	-1.8017	17.9835	1.6155	157	1.0000
L. coleoptrata	Fam	CONVO	FABAC	8.0909	6.0483	-3.8555	20.0373	1.3377	157	1.0000
L. coleoptrata	Fam	CONVO	GENTI	8.0909	7.1381	-6.0082	22.1900	1.1335	157	1.0000
L. coleoptrata	Fam	CONVO	HYPER	8.0909	7.1381	-6.0082	22.1900	1.1335	157	1.0000
L. coleoptrata	Fam	CONVO	MALVA	8.0909	3.6370	0.9071	15.2748	2.2246	157	1.0000
L. coleoptrata	Fam	CONVO	PAPAV	8.0909	4.7128	-1.2177	17.3995	1.7168	157	1.0000
L. coleoptrata	Fam	CONVO	SCROP	-9.7091	5.0084	-19.6017	0.1835	1.9386	157	1.0000
L. coleoptrata	Fam	DIPSA	FABAC	0.0000	6.7814	-13.3946	13.3946	0.0000	157	1.0000
L. coleoptrata	Fam	DIPSA	GENTI	0.0000	7.7691	-15.3455	15.3455	0.0000	157	1.0000
L. coleoptrata	Fam	DIPSA	HYPER	0.0000	7.7691	-15.3455	15.3455	0.0000	157	1.0000
L. coleoptrata	Fam	DIPSA	MALVA	0.0000	4.7576	-9.3971	9.3971	0.0000	157	1.0000
L. coleoptrata	Fam	DIPSA	PAPAV	0.0000	5.6229	-11.1062	11.1062	0.0000	157	1.0000
L. coleoptrata	Fam	DIPSA	SCROP	-17.8000	5.8729	-29.4001	-6.1999	3.0309	157	1.0000
L. coleoptrata	Fam	FABAC	GENTI	0.0000	8.4768	-16.7433	16.7433	0.0000	157	1.0000
L. coleoptrata	Fam	FABAC	HYPER	0.0000	8.4768	-16.7433	16.7433	0.0000	157	1.0000

Table F.4 (cont.) – Results of Fisher's LSD tests comparing ranked abundances of different species of *Xylella fastidiosa* vectors (dependent variable) among classes of environmental factors (independent variable) that showed statistically significant differences (p-value ≤ 0.05) in the one-way ANOVA previously applied. I = class *i* of corresponding independent variable; J = class *j* of corresponding independent variable; I-J = mean difference of ranked abundances between class *i* and class *j*; SE = standard error of I-J; LCL = lower bound of 95% confidence interval; UCL = upper bound of 95% confidence interval; t-value = Fisher's LSD test statistic; df = degrees of freedom. Statistically significant differences (p-value ≤ 0.05) are highlighted in grey.

Dependent variable	Independent variable	I	J	I-J	SE	LCI	UCI	t-value	df	p-value
L. coleoptrata	Fam	FABAC	MALVA	0.0000	5.8422	-11.5395	11.5395	0.0000	157	1.0000
L. coleoptrata	Fam	FABAC	PAPAV	0.0000	6.5661	-12.9693	12.9693	0.0000	157	1.0000
L. coleoptrata	Fam	FABAC	SCROP	-17.8000	6.7814	-31.1946	-4.4054	2.6248	157	1.0000
L. coleoptrata	Fam	GENTI	HYPER	0.0000	9.2859	-18.3414	18.3414	0.0000	157	1.0000
L. coleoptrata	Fam	GENTI	MALVA	0.0000	6.9644	-13.7560	13.7560	0.0000	157	1.0000
L. coleoptrata	Fam	GENTI	PAPAV	0.0000	7.5819	-14.9757	14.9757	0.0000	157	1.0000
L. coleoptrata	Fam	GENTI	SCROP	-17.8000	7.7691	-33.1455	-2.4545	2.2911	157	1.0000
L. coleoptrata	Fam	HYPER	MALVA	0.0000	6.9644	-13.7560	13.7560	0.0000	157	1.0000
L. coleoptrata	Fam	HYPER	PAPAV	0.0000	7.5819	-14.9757	14.9757	0.0000	157	1.0000
L. coleoptrata	Fam	HYPER	SCROP	-17.8000	7.7691	-33.1455	-2.4545	2.2911	157	1.0000
L. coleoptrata	Fam	MALVA	PAPAV	0.0000	4.4453	-8.7803	8.7803	0.0000	157	1.0000
L. coleoptrata	Fam	MALVA	SCROP	-17.8000	4.7576	-27.1971	-8.4029	3.7414	157	0.0003
L. coleoptrata	Fam	PAPAV	SCROP	-17.8000	5.6229	-28.9062	-6.6938	3.1656	157	0.0019
N. campestris	Vine250	0	]0,25]	2.2556	3.8677	-5.3879	9.8992	0.5832	147	0.5607
N. campestris	Vine250	0	]25,50]	-16.4944	6.7543	-29.8425	-3.1462	2.4420	147	0.0158
N. campestris	Vine250	]0,25]	]25,50]	-18.7500	7.6103	-33.7897	-3.7103	2.4638	147	0.0149
N. campestris	Cork250	0	]0,25]	-7.7705	2.9149	-13.5311	-2.0099	2.6657	147	0.0085
N. campestris	Cork250	0	]0,25]	1.2295	7.7595	-14.1052	16.5642	0.1585	147	0.8743
N. campestris	Cork250	]0,25]	]25,50]	9.0000	8.1128	-7.0328	25.0328	1.1094	147	0.2691
Philaenus sp.	GU	0	1	9.1875	10.5147	-11.6116	29.9866	0.8738	132	0.3838
Philaenus sp.	GU	0	2	9.1875	6.8835	-4.4287	22.8037	1.3347	132	0.1843
Philaenus sp.	GU	0	3	9.1875	12.2785	-15.1006	33.4756	0.7483	132	0.4556
Philaenus sp.	GU	0	4	-27.5625	12.2785	-51.8506	-3.2744	2.2448	132	0.0264
Philaenus sp.	GU	0	6	-18.7500	7.7656	-34.1111	-3.3889	2.4145	132	0.0171
Philaenus sp.	GU	0	7	-27.5625	12.2785	-51.8506	-3.2744	2.2448	132	0.0264
Philaenus sp.	GU	0	8	9.1875	6.8835	-4.4287	22.8037	1.3347	132	0.1843
Philaenus sp.	GU	0	9	3.6161	6.8835	-10.0001	17.2323	0.5253	132	0.6002
Philaenus sp.	GU	0	13	9.1875	7.5468	-5.7408	24.1158	1.2174	132	0.2256
Philaenus sp.	GU	0	14	9.1875	8.0382	-6.7128	25.0878	1.1430	132	0.2551
Philaenus sp.	GU	0	15	3.6161	6.8835	-10.0001	17.2323	0.5253	132	0.6002
Philaenus sp.	GU	0	19	9.1875	7.5468	-5.7408	24.1158	1.2174	132	0.2256
Philaenus sp.	GU	0	20	9.1875	7.5468	-5.7408	24.1158	1.2174	132	0.2256
Philaenus sp.	GU	0	21	9.1875	7.7656	-6.1736	24.5486	1.1831	132	0.2389
Philaenus sp.	GU	0	25	9.1875	7.7656	-6.1736	24.5486	1.1831	132	0.2389
Philaenus sp.	GU	0	26	9.1875	7.5468	-5.7408	24.1158	1.2174	132	0.2256
Philaenus sp.	GU	0	27	9.1875	7.3671	-5.3853	23.7603	1.2471	132	0.2146
Philaenus sp.	GU	1	2	0.0000	9.8811	-19.5458	19.5458	0.0000	132	1.0000
Philaenus sp.	GU	1	3	0.0000	14.1780	-28.0454	28.0454	0.0000	132	1.0000
Philaenus sp.	GU	1	4	-36.7500	14.1780	-64.7954	-8.7046	2.5920	132	0.0106
Philaenus sp.	GU	1	6	-27.9375	10.5147	-48.7366	-7.1384	2.6570	132	0.0089
Philaenus sp.	GU	1	7	-36.7500	14.1780	-64.7954	-8.7046	2.5920	132	0.0106
Philaenus sp.	GU	1	8	0.0000	9.8811	-19.5458	19.5458	0.0000	132	1.0000
Philaenus sp.	GU	1	9	-5.5714	9.8811	-25.1172	13.9743	0.5638	132	0.5738
Philaenus sp.	GU	1	13	0.0000	10.3541	-20.4815	20.4815	0.0000	132	1.0000
Philaenus sp.	GU	1	14	0.0000	10.7176	-21.2004	21.2004	0.0000	132	1.0000
Philaenus sp.	GU	1	15	-5.5714	9.8811	-25.1172	13.9743	0.5638	132	0.5738
Philaenus sp.	GU	1	19	0.0000	10.3541	-20.4815	20.4815	0.0000	132	1.0000
Philaenus sp.	GU	1	20	0.0000	10.3541	-20.4815	20.4815	0.0000	132	1.0000
Philaenus sp.	GU	1	21	0.0000	10.5147	-20.7991	20.7991	0.0000	132	1.0000
Philaenus sp.	GU	1	25	0.0000	10.5147	-20.7991	20.7991	0.0000	132	1.0000

Table F.4 (cont.) – Results of Fisher's LSD tests comparing ranked abundances of different species of *Xylella fastidiosa* vectors (dependent variable) among classes of environmental factors (independent variable) that showed statistically significant differences (p-value ≤ 0.05) in the one-way ANOVA previously applied. I = class *i* of corresponding independent variable; J = class *j* of corresponding independent variable; I-J = mean difference of ranked abundances between class *i* and class *j*; SE = standard error of I-J; LCL = lower bound of 95% confidence interval; UCL = upper bound of 95% confidence interval; t-value = Fisher's LSD test statistic; df = degrees of freedom. Statistically significant differences (p-value ≤ 0.05) are highlighted in grey.

Dependent variable	Independent variable	I	J	I-J	SE	LCI	UCI	t-value	df	p-value
Philaenus sp.	GU	1	26	0.0000	10.3541	-20.4815	20.4815	0.0000	132	1.0000
Philaenus sp.	GU	1	27	0.0000	10.2239	-20.2239	20.2239	0.0000	132	1.0000
Philaenus sp.	GU	2	3	0.0000	11.7405	-23.2238	23.2238	0.0000	132	1.0000
Philaenus sp.	GU	2	4	-36.7500	11.7405	-59.9738	-13.5262	3.1302	132	0.0022
Philaenus sp.	GU	2	6	-27.9375	6.8835	-41.5537	-14.3213	4.0586	132	0.0001
Philaenus sp.	GU	2	7	-36.7500	11.7405	-59.9738	-13.5262	3.1302	132	0.0022
Philaenus sp.	GU	2	8	0.0000	5.8702	-11.6119	11.6119	0.0000	132	1.0000
Philaenus sp.	GU	2	9	-5.5714	5.8702	-17.1833	6.0405	0.9491	132	0.3443
Philaenus sp.	GU	2	13	0.0000	6.6357	-13.1260	13.1260	0.0000	132	1.0000
Philaenus sp.	GU	2	14	0.0000	7.1895	-14.2216	14.2216	0.0000	132	1.0000
Philaenus sp.	GU	2	15	-5.5714	5.8702	-6.0405	17.1833	0.9491	132	0.3443
Philaenus sp.	GU	2	19	0.0000	6.6357	-13.1260	13.1260	0.0000	132	1.0000
Philaenus sp.	GU	2	20	0.0000	6.6357	-13.1260	13.1260	0.0000	132	1.0000
Philaenus sp.	GU	2	21	0.0000	6.8835	-13.6162	13.6162	0.0000	132	1.0000
Philaenus sp.	GU	2	25	0.0000	6.8835	-13.6162	13.6162	0.0000	132	1.0000
Philaenus sp.	GU	2	26	0.0000	6.6357	-13.1260	13.1260	0.0000	132	1.0000
Philaenus sp.	GU	2	27	0.0000	6.4305	-12.7202	12.7202	0.0000	132	1.0000
Philaenus sp.	GU	3	4	-36.7500	15.5312	-67.4722	-6.0278	2.3662	132	0.0194
Philaenus sp.	GU	3	6	-27.9375	12.2785	-52.2256	-3.6494	2.2753	132	0.0245
Philaenus sp.	GU	3	7	-36.7500	15.5312	-67.4722	-6.0278	2.3662	132	0.019
Philaenus sp.	GU	3	8	0.0000	11.7405	-23.2238	23.2238	0.0000	132	1.0000
Philaenus sp.	GU	3	9	-5.5714	11.7405	-28.7953	17.6524	0.4745	132	0.6359
Philaenus sp.	GU	3	13	0.0000	12.1413	-24.0167	24.0167	0.0000	132	1.0000
Philaenus sp.	GU	3	14	0.0000	12.4527	-24.6326	24.6326	0.0000	132	1.0000
Philaenus sp.	GU	3	15	-5.5714	11.7405	-17.6524	28.7953	0.4745	132	0.6359
Philaenus sp.	GU	3	19	0.0000	12.1413	-24.0167	24.0167	0.0000	132	1.0000
Philaenus sp.	GU	3	20	0.0000	12.1413	-24.0167	24.0167	0.0000	132	1.0000
Philaenus sp.	GU	3	21	0.0000	12.2785	-24.2881	24.2881	0.0000	132	1.0000
Philaenus sp.	GU	3	25	0.0000	12.2785	-24.2881	24.2881	0.0000	132	1.0000
Philaenus sp.	GU	3	26	0.0000	12.1413	-24.0167	24.0167	0.0000	132	1.0000
Philaenus sp.	GU	3	27	0.0000	12.0304	-23.7974	23.7974	0.0000	132	1.0000
Philaenus sp.	GU	4	6	8.8125	12.2785	-15.4756	33.1006	0.7177	132	0.4742
Philaenus sp.	GU	4	7	0.0000	15.5312	-30.7222	30.7222	0.0000	132	1.0000
Philaenus sp.	GU	4	8	36.7500	11.7405	13.5262	59.9738	3.1302	132	0.0022
Philaenus sp.	GU	4	9	31.1786	11.7405	7.9547	54.4024	2.6556	132	0.0089
Philaenus sp.	GU	4	13	36.7500	12.1413	-60.7667	-12.7333	3.0269	132	0.0030
Philaenus sp.	GU	4	14	36.7500	12.4527	-61.3826	-12.1174	2.9512	132	0.0037
Philaenus sp.	GU	4	15	31.1786	11.7405	-54.4024	-7.9547	2.6556	132	0.0089
Philaenus sp.	GU	4	19	36.7500	12.1413	-60.7667	-12.7333	3.0269	132	0.0030
Philaenus sp.	GU	4	20	36.7500	12.1413	-60.7667	-12.7333	3.0269	132	0.0030
Philaenus sp.	GU	4	21	36.7500	12.2785	-61.0381	-12.4619	2.9930	132	0.0033
Philaenus sp.	GU	4	25	36.7500	12.2785	-61.0381	-12.4619	2.9930	132	0.0033
Philaenus sp.	GU	4	26	36.7500	12.1413	-60.7667	-12.7333	3.0269	132	0.0030
Philaenus sp.	GU	4	27	36.7500	12.0304	-60.5474	-12.9527	3.0548	132	0.0027
Philaenus sp.	GU	6	7	-8.8125	12.2785	-33.1006	15.4756	0.7177	132	0.4742
Philaenus sp.	GU	6	8	27.9375	6.8835	14.3213	41.5537	4.0586	132	0.0001
Philaenus sp.	GU	6	9	22.3661	6.8835	8.7499	35.9823	3.2492	132	0.0015
Philaenus sp.	GU	6	13	27.9375	7.5468	-42.8658	-13.0092	3.7019	132	0.0003
Philaenus sp.	GU	6	14	27.9375	8.0382	-43.8378	-12.0372	3.4756	132	0.0007
Philaenus sp.	GU	6	15	22.3661	6.8835	-35.9823	-8.7499	3.2492	132	0.0015

Table F.4 (cont.) – Results of Fisher's LSD tests comparing ranked abundances of different species of *Xylella fastidiosa* vectors (dependent variable) among classes of environmental factors (independent variable) that showed statistically significant differences (p-value ≤ 0.05) in the one-way ANOVA previously applied. I = class *i* of corresponding independent variable; J = class *j* of corresponding independent variable; I-J = mean difference of ranked abundances between class *i* and class *j*; SE = standard error of I-J; LCL = lower bound of 95% confidence interval; UCL = upper bound of 95% confidence interval; t-value = Fisher's LSD test statistic; df = degrees of freedom. Statistically significant differences (p-value ≤ 0.05) are highlighted in grey.

Dependent variable	Independent variable	I	J	I-J	SE	LCI	UCI	t-value	df	p-value
Philaenus sp.	GU	6	19	27.9375	7.5468	-42.8658	-13.0092	3.7019	132	0.0003
Philaenus sp.	GU	6	20	27.9375	7.5468	-42.8658	-13.0092	3.7019	132	0.0003
Philaenus sp.	GU	6	21	27.9375	7.7656	-43.2986	-12.5764	3.5976	132	0.0005
Philaenus sp.	GU	6	25	27.9375	7.7656	-43.2986	-12.5764	3.5976	132	0.0005
Philaenus sp.	GU	6	26	27.9375	7.5468	-42.8658	-13.0092	3.7019	132	0.0003
Philaenus sp.	GU	6	27	27.9375	7.3671	-42.5103	-13.3647	3.7922	132	0.0002
Philaenus sp.	GU	7	8	36.7500	11.7405	13.5262	59.9738	3.1302	132	0.0022
Philaenus sp.	GU	7	9	31.1786	11.7405	7.9547	54.4024	2.6556	132	0.0089
Philaenus sp.	GU	7	13	36.7500	12.1413	-60.7667	-12.7333	3.0269	132	0.0030
Philaenus sp.	GU	7	14	36.7500	12.4527	-61.3826	-12.1174	2.9512	132	0.0037
Philaenus sp.	GU	7	15	31.1786	11.7405	-54.4024	-7.9547	2.6556	132	0.0089
Philaenus sp.	GU	7	19	36.7500	12.1413	-60.7667	-12.7333	3.0269	132	0.0030
Philaenus sp.	GU	7	20	36.7500	12.1413	-60.7667	-12.7333	3.0269	132	0.0030
Philaenus sp.	GU	7	21	36.7500	12.2785	-61.0381	-12.4619	2.9930	132	0.0033
Philaenus sp.	GU	7	25	36.7500	12.2785	-61.0381	-12.4619	2.9930	132	0.0033
Philaenus sp.	GU	7	26	36.7500	12.1413	-60.7667	-12.7333	3.0269	132	0.0030
Philaenus sp.	GU	7	27	36.7500	12.0304	-60.5474	-12.9527	3.0548	132	0.0027
Philaenus sp.	GU	8	9	-5.5714	5.8702	-17.1833	6.0405	0.9491	132	0.3443
Philaenus sp.	GU	8	13	0.0000	6.6357	-13.1260	13.1260	0.0000	132	1.0000
Philaenus sp.	GU	8	14	0.0000	7.1895	-14.2216	14.2216	0.0000	132	1.0000
Philaenus sp.	GU	8	15	-5.5714	5.8702	-6.0405	17.1833	0.9491	132	0.3443
Philaenus sp.	GU	8	19	0.0000	6.6357	-13.1260	13.1260	0.0000	132	1.0000
Philaenus sp.	GU	8	20	0.0000	6.6357	-13.1260	13.1260	0.0000	132	1.0000
Philaenus sp.	GU	8	21	0.0000	6.8835	-13.6162	13.6162	0.0000	132	1.0000
Philaenus sp.	GU	8	25	0.0000	6.8835	-13.6162	13.6162	0.0000	132	1.0000
Philaenus sp.	GU	8	26	0.0000	6.6357	-13.1260	13.1260	0.0000	132	1.0000
Philaenus sp.	GU	8	27	0.0000	6.4305	-12.7202	12.7202	0.0000	132	1.0000
Philaenus sp.	GU	9	13	5.5714	6.6357	-18.6974	7.5545	0.8396	132	0.4026
Philaenus sp.	GU	9	14	5.5714	7.1895	-19.7931	8.6502	0.7749	132	0.4398
Philaenus sp.	GU	9	15	0.0000	5.8702	-11.6119	11.6119	0.0000	132	1.0000
Philaenus sp.	GU	9	19	5.5714	6.6357	-18.6974	7.5545	0.8396	132	0.4026
Philaenus sp.	GU	9	20	5.5714	6.6357	-18.6974	7.5545	0.8396	132	0.4026
Philaenus sp.	GU	9	21	5.5714	6.8835	-19.1876	8.0448	0.8094	132	0.4197
Philaenus sp.	GU	9	25	5.5714	6.8835	-19.1876	8.0448	0.8094	132	0.4197
Philaenus sp.	GU	9	26	5.5714	6.6357	-18.6974	7.5545	0.8396	132	0.4026
Philaenus sp.	GU	9	27	5.5714	6.4305	-18.2916	7.1488	0.8664	132	0.3878
Philaenus sp.	GU	13	14	0.0000	7.8270	-15.4826	15.4826	0.0000	132	1.0000
Philaenus sp.	GU	13	15	-5.5714	6.6357	-18.6974	7.5545	0.8396	132	0.4026
Philaenus sp.	GU	13	19	0.0000	7.3215	-14.4826	14.4826	0.0000	132	1.0000
Philaenus sp.	GU	13	20	0.0000	7.3215	-14.4826	14.4826	0.0000	132	1.0000
Philaenus sp.	GU	13	21	0.0000	7.5468	-14.9283	14.9283	0.0000	132	1.0000
Philaenus sp.	GU	13	25	0.0000	7.5468	-14.9283	14.9283	0.0000	132	1.0000
Philaenus sp.	GU	13	26	0.0000	7.3215	-14.4826	14.4826	0.0000	132	1.0000
Philaenus sp.	GU	13	27	0.0000	7.1361	-14.1159	14.1159	0.0000	132	1.0000
Philaenus sp.	GU	14	15	-5.5714	7.1895	-19.7931	8.6502	0.7749	132	0.4398
Philaenus sp.	GU	14	19	0.0000	7.8270	-15.4826	15.4826	0.0000	132	1.0000
Philaenus sp.	GU	14	20	0.0000	7.8270	-15.4826	15.4826	0.0000	132	1.0000
Philaenus sp.	GU	14	21	0.0000	8.0382	-15.9003	15.9003	0.0000	132	1.0000
Philaenus sp.	GU	14	25	0.0000	8.0382	-15.9003	15.9003	0.0000	132	1.0000
Philaenus sp.	GU	14	26	0.0000	7.8270	-15.4826	15.4826	0.0000	132	1.0000

Table F.4 (cont.) – Results of Fisher's LSD tests comparing ranked abundances of different species of *Xylella fastidiosa* vectors (dependent variable) among classes of environmental factors (independent variable) that showed statistically significant differences (p-value ≤ 0.05) in the one-way ANOVA previously applied. I = class *i* of corresponding independent variable; J = class *j* of corresponding independent variable; I-J = mean difference of ranked abundances between class *i* and class *j*; SE = standard error of I-J; LCL = lower bound of 95% confidence interval; UCL = upper bound of 95% confidence interval; t-value = Fisher's LSD test statistic; df = degrees of freedom. Statistically significant differences (p-value ≤ 0.05) are highlighted in grey.

Dependent variable	Independent variable	I	J	I-J	SE	LCI	UCI	t-value	df	p-value
Philaenus sp.	GU	14	27	0.0000	7.6539	-15.1401	15.1401	0.0000	132	1.0000
Philaenus sp.	GU	15	19	5.5714	6.6357	-7.5545	18.6974	0.8396	132	0.4026
Philaenus sp.	GU	15	20	5.5714	6.6357	-7.5545	18.6974	0.8396	132	0.4026
Philaenus sp.	GU	15	21	5.5714	6.8835	-8.0448	19.1876	0.8094	132	0.4197
Philaenus sp.	GU	15	25	5.5714	6.8835	-8.0448	19.1876	0.8094	132	0.4197
Philaenus sp.	GU	15	26	5.5714	6.6357	-7.5545	18.6974	0.8396	132	0.4026
Philaenus sp.	GU	15	27	5.5714	6.4305	-7.1488	18.2916	0.8664	132	0.3878
Philaenus sp.	GU	19	20	0.0000	7.3215	-14.4826	14.4826	0.0000	132	1.0000
Philaenus sp.	GU	19	21	0.0000	7.5468	-14.9283	14.9283	0.0000	132	1.0000
Philaenus sp.	GU	19	25	0.0000	7.5468	-14.9283	14.9283	0.0000	132	1.0000
Philaenus sp.	GU	19	26	0.0000	7.3215	-14.4826	14.4826	0.0000	132	1.0000
Philaenus sp.	GU	19	27	0.0000	7.1361	-14.1159	14.1159	0.0000	132	1.0000
Philaenus sp.	GU	20	21	0.0000	7.5468	-14.9283	14.9283	0.0000	132	1.0000
Philaenus sp.	GU	20	25	0.0000	7.5468	-14.9283	14.9283	0.0000	132	1.0000
Philaenus sp.	GU	20	26	0.0000	7.3215	-14.4826	14.4826	0.0000	132	1.0000
Philaenus sp.	GU	20	27	0.0000	7.1361	-14.1159	14.1159	0.0000	132	1.0000
Philaenus sp.	GU	21	25	0.0000	7.7656	-15.3611	15.3611	0.0000	132	1.0000
Philaenus sp.	GU	21	26	0.0000	7.5468	-14.9283	14.9283	0.0000	132	1.0000
Philaenus sp.	GU	21	27	0.0000	7.3671	-14.5728	14.5728	0.0000	132	1.0000
Philaenus sp.	GU	25	26	0.0000	7.5468	-14.9283	14.9283	0.0000	132	1.0000
Philaenus sp.	GU	25	27	0.0000	7.3671	-14.5728	14.5728	0.0000	132	1.0000
Philaenus sp.	GU	26	27	0.0000	7.1361	-14.1159	14.1159	0.0000	132	1.0000
Philaenus sp.	Tmed	19	21	-2.3284	3.5469	-9.3386	4.6819	0.6565	145	0.5126
Philaenus sp.	Tmed	19	24	-21.2143	5.2259	-31.543	-10.8856	4.0595	145	0.0001
Philaenus sp.	Tmed	19	26	-3.8684	3.9433	-11.6622	3.9253	0.981	145	0.3282
Philaenus sp.	Tmed	21	24	-18.8859	4.7446	-28.2634	-9.5085	3.9805	145	0.0001
Philaenus sp.	Tmed	21	26	-1.5401	3.2788	-8.0206	4.9405	0.4697	145	0.6393
Philaenus sp.	Tmed	24	26	17.3459	5.0478	7.3691	27.3226	3.4363	145	0.0008
Philaenus sp.	Oliv250	0	]0,25]	-4.7553	3.5882	-11.8476	2.3369	1.3253	144	0.1872
Philaenus sp.	Oliv250	0	]25,50]	-2.5345	4.0491	-10.5377	5.4688	0.6259	144	0.5323
Philaenus sp.	Oliv250	0	]50,75]	-17.8235	4.7836	-27.2786	-8.3684	3.7260	144	0.0003
Philaenus sp.	Oliv250	0	]75,100]	0.0000	4.7836	-9.4551	9.4551	0.0000	144	1.0000
Philaenus sp.	Oliv250	0	100	0.0000	9.8005	-19.3715	19.3715	0.0000	144	1.0000
Philaenus sp.	Oliv250	]0,25]	]25,50]	2.2208	3.8551	-5.3991	9.8408	0.5761	144	0.5655
Philaenus sp.	Oliv250	]0,25]	]50,75]	-13.0682	4.6206	-22.2012	-3.9352	2.8282	144	0.0053
Philaenus sp.	Oliv250	]0,25]	]75,100]	4.7553	4.6206	-4.3776	13.8883	1.0292	144	0.3051
Philaenus sp.	Oliv250	]0,25]	100	4.7553	9.7220	-14.4610	23.9717	0.4891	144	0.6255
Philaenus sp.	Oliv250	]25,50]	]50,75]	-15.289	4.9870	-25.1462	-5.4319	3.0658	144	0.0026
Philaenus sp.	Oliv250	]25,50]	]75,100]	2.5345	4.9870	-7.3227	12.3916	0.5082	144	0.6121
Philaenus sp.	Oliv250	]25,50]	100	2.5345	9.9014	-17.0364	22.1054	0.2560	144	0.7983
Philaenus sp.	Oliv250	]50,75]	]75,100]	17.8235	5.5998	6.7551	28.8920	3.1829	144	0.0018
Philaenus sp.	Oliv250	]50,75]	100	17.8235	10.2238	-2.3846	38.0316	1.7433	144	0.0834
Philaenus sp.	Oliv250	]75,100]	100	0.0000	10.2238	-20.2081	20.2081	0.0000	144	1.0000
P. tesselatus	Prec	5	10	-28.5121	8.9128	10.8974	46.1269	3.1990	146	0.0017
P. tesselatus	Prec	5	25	-9.2253	7.4839	-5.5655	24.0161	1.2327	146	0.2197
P. tesselatus	Prec	5	50	-17.9833	6.8369	-31.4954	-4.4712	2.6303	146	0.0094
P. tesselatus	Prec	10	25	19.2868	8.6887	2.1150	36.4587	2.2198	146	0.0280
P. tesselatus	Prec	10	50	10.5288	8.1381	-5.5548	26.6124	1.2938	146	0.1978
P. tesselatus	Prec	25	50	-8.7580	6.5421	-21.6874	4.1714	1.3387	146	0.1827
P. tesselatus	Oliv250	0	]0,25]	20.7625	6.9700	6.9858	34.5392	2.9789	144	0.0034

Table F.4 (cont.) – Results of Fisher's LSD tests comparing ranked abundances of different species of Xylella fastidiosa vectors *(dependent* variable) among classes of environmental factors (independent variable) that showed statistically significant differences (p-value ≤ 0.05) in the one-way ANOVA previously applied. I = class i of corresponding independent variable; J = class j of corresponding independent variable; I-J = mean difference of ranked abundances between class i and class j; SE = standard error of I-J; LCL = lower bound of 95% confidence interval; UCL = upper bound of 95% confidence interval; t-value = Fisher's LSD test statistic; df = degrees of freedom. Statistically significant differences (p-value ≤ 0.05) are highlighted in grey.

Dependent variable	Independent variable	I	J	I-J	SE	LCI	UCI	t-value	df	p-value
P. tesselatus	Oliv250	0	]25,50]	7.0252	7.8653	-8.5211	22.5715	0.8932	144	0.3732
P. tesselatus	Oliv250	0	]50,75]	20.4897	9.2921	2.1232	38.8562	2.2051	144	0.0290
P. tesselatus	Oliv250	0	]75,100]	8.8426	9.2921	-9.5239	27.2091	0.9516	144	0.3429
P. tesselatus	Oliv250	0	100	29.7838	19.0375	-7.8453	67.4128	1.5645	144	0.1199
P. tesselatus	Oliv250	]0,25]	]25,50]	-13.7373	7.4886	-28.5391	1.0644	1.8344	144	0.0687
P. tesselatus	Oliv250	]0,25]	]50,75]	-0.2728	8.9755	-18.0136	17.4679	0.0304	144	0.9758
P. tesselatus	Oliv250	]0,25]	]75,100]	-11.9199	8.9755	-29.6606	5.8208	1.3281	144	0.1863
P. tesselatus	Oliv250	]0,25]	100	9.0213	18.885	-28.3063	46.3489	0.4777	144	0.6336
P. tesselatus	Oliv250	]25,50]	]50,75]	13.4645	9.6872	-5.6829	32.6119	1.3899	144	0.1667
P. tesselatus	Oliv250	]25,50]	]75,100]	1.8174	9.6872	-17.3300	20.9649	0.1876	144	0.8514
P. tesselatus	Oliv250	]25,50]	100	22.7586	19.2334	-15.2577	60.7749	1.1833	144	0.2386
P. tesselatus	Oliv250	]50,75]	]75,100]	-11.6471	10.8776	-33.1474	9.8533	1.0707	144	0.2861
P. tesselatus	Oliv250	]50,75]	100	9.2941	19.8596	-29.9599	48.5482	0.4680	144	0.6405
P. tesselatus	Oliv250	]75,100]	100	20.9412	19.8596	-18.3129	60.1952	1.0545	144	0.2934